

1 CGGGCAGCAA AGGAGGGATGG CGAGGGGCTG ATACTGAACC CGGGAAAGGT
51 GGGCTGTGCT GAAGCTAGAG CCGGAGCCGG AGCTGGGGCC AGAACCCGAG
101 CACTGCCATG TCCACGCAGA GACTTCGAA TGAAAGTAC CACGACTACA
151 GCTCCACCGGA CGTGAGCCCT GAGGAGAGCC CGTCGGAAGG CCTCAACAAAC
201 CTCTCTCTCC CGGGCTCTTA CCAGCGCTTT GGTCAAAGCA ATAGCACAAAC
251 ATGGTTTCAAG ACCTTGATCC ACCTGTTAAA AGGCAACATT GGACAGGAC
301 TCCTGGGACT CCCCTCTGGGG GTGAAAAAAT CAGGCATCGT GATGGGTCCC
351 ATCAGCCTGC TGATCATAGG CATCGTGGCC GTGCACTGCA TGGGTATCCT
401 GGTGAAATGT GCTCACCACT TCTGCCCCAG GCTGAATAAA TCCCTTGTGG
451 ATTATGGTGA TACTGTGATG TATGGACTAG AATCCAGCCC CTGCTCTGG
501 CTCCCGAACCT ACGCACACTG GGGAAAGACGT GTTGTGGACT TCTTCTGTGAT
551 TGTCAACCGAG CTGGGATTCT GTCTGTGCTA TTTTGTGTTT CTGGCTGACA
601 ACTTTAAACA GGTGATAGAA GCGGCGCAAT GGACCAACAA TAACGTCCAC
651 AACAAATGAGA CGGTGATTCT GACGCCATAC ATGGACTCGC GACTCTACAT
701 GCTCTCTTC CGTCCCCCTCC TTGGTGTGCT GGTTTTCATC AGGAACCTCC
751 GAGCCCTGTC CATCTTCTCC CTGTTGGCCA ACATCACTAT GCTGGTCAGC
801 TTGGTCTATG TCTACCACTG CATTGGTCAG AGGATCCCGAG ACCCCAGCCA
851 CCTCCCCCTG GTGGCCCCCTT GGGAGACCTA CCCTCTCTC TTTGGCACAG
901 CGATTTTTTC ATTTGAAAGG ATTTGGAATGG TTCTGCCCCT GGAAAACAAA
951 ATGAAAGGATC CTGGGAAGT CCAACTCATC CTGTAACCTGG GCATGGTCAT
1001 CGTCACCATC CTCTACATCA GCGCTGGGGTG TCTGGGGTAC CTGCAATTG
1051 GAGCTAATAT CCAAGGCAGC ATAACCTCTA ACCTGCCCCA CTGCTGGTTG
1101 TACCACTGAG TTAAGCTGCT GTACTCCATC GGATCTTTT TCACCTACGC
1151 ACTCCAGTTC TACGTCCCCGG CTAGAGATCAT CATCCCCCTC TTTGTGTCCC
1201 GAGCGCCCGA GCACTGTGAG TTAGTGGTGG ACCTGTTTGT GCGCACAGTG
1251 CTGGCTGCG TGACATGCACT TTGGGACATC CTACATCCCCC GCCTGGACCT
1301 GGTTCATCTCC CTGGTGGGGT CCGTGGAGCAG CAGCGCCCTG GCCCTCATCA
1351 TCCCACCGCT CCTGGAGGTC ACCACCTCT ACTCAGAGGG CATGAGCCCC
1401 CTACCATCTT TTAAGGGACG CCGTACATC ATCCTGGGCT TCCTGGGCTT
1451 TGTGGTGGGG ACCTATGAGG CTCTCTATGA GCTGTATCAG CCAAGCAATG
1501 CTCCCATCTT CATCAATTCC ACCTGTGCC TCAATAGGG ATCTGGGTT
1551 GTCTCTGCAC CTGCTTACCC CTGCCCCATG TGCCCCCGT TACCTGTCT
1601 CGAGGCCCTA GGTATGGTCC AGGCTCTGAG GAAAGTCAGG GTTGTGTG
1651 GGGAAACCCCT CTGCCCTGGCA CCTGGATACCC CTGGGCCAGG TAACCTGAGG
1701 GCAGGGGAGA GGTGGGGTGG CAGACACGCC GAAGTGCTAC TAGTGACAGG
1751 GCTGCCATCG CTCACCTGTA CCTATTACA CCCAGAACCT TCCAGCTCCC
1801 CCTCATCATG CCTCCCTCTT CCTACCTGCC TCCCCTCTGC TGGTGCACCT
1851 CGCCCAACTC ATTCTTACTG CACAGTTCAC TTATTTAAC AATTTTCATG
1901 TCCCCCATCT CGCTCTGTGC CCCTCCCTCAC CAGGGCTTCA GCAGGAGCCC
1951 TGGACTCATC ATCAATAAAC ACTGTTACAG CAAAAAAAGA AAAAAAAAGA
2001 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAGA
2051 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA (SEQ ID NO:1)

FEATURES:
5'UTR: 1-107
Start Codon: 108
Stop Codon: 1536
3'UTR: 1539

FIGURE 1A

Docket No.: CL001062CON
Serial No.: TO BE ASSIGNED
Inventors: WEI, Ming-Hui et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

				Score	E
CRA	89000000199482	/altid=gi 7297404	/def=gb AAF52663.1 (AE003...	330	4e-89
CRA	89000000199480	/altid=gi 7297402	/def=gb AAF52661.1 (AE003...	330	4e-89
CRA	89000000199481	/altid=gi 7297403	/def=gb AAF52662.1 (AE003...	330	4e-89
CRA	89000000197173	/altid=gi 7294781	/def=gb AAF50116.1 (AE003...	268	1e-70
CRA	89000000195851	/altid=gi 7293314	/def=gb AAF48694.1 (AE003...	265	1e-69
CRA	18000005127815	/altid=gi 7509795	/def=pir T26845 hypothetical	258	2e-67
CRA	89000000194855	/altid=gi 7292192	/def=gb AAF47603.1 (AE003...	253	5e-66
CRA	89000000197171	/altid=gi 7294779	/def=gb AAF50114.1 (AE003...	252	8e-66
CRA	89000000197172	/altid=gi 7294780	/def=gb AAF50115.1 (AE003...	252	8e-66
CRA	18000005102492	/altid=gi 2429516	/def=gb AAB71045.1 (AF025...	250	3e-65

BLAST dbEST hits:

		Score	E
gi	5422591 /dataset=dbest /taxon=9606 ...	1400	0.0
gi	3648072 /dataset=dbest /taxon=9606 ...	1017	0.0
gi	5746200 /dataset=dbest /taxon=9606 ...	730	0.0
gi	10249244 /dataset=dbest /taxon=960... ...	642	0.0
gi	8612353 /dataset=dbest /taxon=960... ...	329	1e-87
gi	10083945 /dataset=dbest /taxon=960... ...	313	7e-83

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|5422591 testis
gi|3648072 Testis
gi|5746200 Brain meningiomas
gi|10249244 Brain normal
gi|8612353 Head-neck
gi|10083945 Colon

From tissue screening panels:

Human Whole Liver

FIGURE 1B

```

1 MSTQRLRNED YHDYSSTDVS PEEPSSEGLN NLSSPGSYQR FGQSNSTTWF
51 QTLIHLLKGN IGTGGLLGPL AVKNAGIVMG PISLLIIGIV AVHCMGILVK
101 CAHHFCRRLN KSFVDYGDVT MYGLESSPCs WLRNHAHWGR RVVDFFLIVT
151 QLGFCVVFV FLADNFQKV EAANGTTNNC HNNETVILTP TMDSRLYMLS
201 FLPFLVLLVF IRNLRALSIF SLLANITMLV SLVMIQFIV QRIPDPSHLP
251 LVAPWKTYPL FFGTAIFSFE GIGMVLPLEN KMKDPRKFPL ILYLGIVT
301 ILYISLGCLG YLQFGGANIQG SITLNLPNCW LYQSVKLLYS IGIFFTYALQ
351 FYVPAEIIIP FFVSRAPEHC ELVVDLFVRT VLVCILCILA ILIPRLDLVI
401 SLVGSVSSSA LAIIPPLLE VTTFYSEGMS PLTIFKDALI SILGFVGFVV
451 GTYEALYELI QPSNAPIFIN STCAFI (SEQ ID NO:2)

```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
 N-glycosylation site

Number of matches: 7

1	31-34	NLSS
2	45-48	NSTT
3	110-113	NKSF
4	174-177	NGTT
5	183-186	NETV
6	225-228	NITM
7	470-473	NSTC

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
 Protein kinase C phosphorylation site

Number of matches: 2

1	3-5	TQR
2	334-336	SVK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
 Casein kinase II phosphorylation site

Number of matches: 4

1	15-18	SSTD
2	20-23	SPEE
3	24-27	SPSE
4	112-115	SFVD

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
 Tyrosine kinase phosphorylation site

7-14 RNEDYHDY

[5] PDOC00008 PS00008 MYRISTYL
 N-myristoylation site

Number of matches: 7

1	42-47	GQSNST
2	59-64	GNIGTG
3	67-72	GPLAV
4	175-180	GTTNNC
5	342-347	GIFFTY
6	404-409	GSVSSS
7	451-456	GTYEAL

[6] PDOC00009 PS00009 AMIDATION
 Amidation site

138-141 WGRR

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	52	72	0.668	Putative
2	75	95	2.032	Certain
3	143	163	1.799	Certain

FIGURE 2A

Docket No.: CL001062CON
Serial No.: TO BE ASSIGNED
Inventors: WEI, Ming-Hui et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

4	193	213	1.467	Certain
5	216	236	1.884	Certain
6	258	278	1.566	Certain
7	289	309	2.126	Certain
8	335	355	1.378	Certain
9	375	395	1.332	Certain
10	398	418	1.748	Certain
11	437	457	1.533	Certain

FIGURE 2B

BLAST Alignment to Top Hit:

>CRA|89000000199482 /altid=gi|7297404 /def=gb|AAF52663.1| (AE003621)
CG13384 gene product [alt 3] [prosophila melanogaster]
/org=Drosophila melanogaster /taxon=7227 /dataset=nraa
/length=486
Length = 486

Score = 330 bits (837), Expect = 2e-89
Identities = 184/425 (43%), Positives = 262/425 (61%), Gaps = 32/425 (7%)

Query: 47 TTWFQTLIHLLKGNI GTGLLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFC 106
T+ F TL+HLLKGNI GTG+L +P A KNAG+ +G +I+G + HCM +LV C+H C
Sbjct: 78 TSNFDTLVHLLKGNI GTGILAMPDAFKNAGLYVGLFGTMIMGAICTHCMHMLVNCSEL 137

Query: 107 RRLNKSFVDYGD TVMYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCCVYFVFLADNF 166
RR + +D+ + ES P LR ++ RR+V FL +TQ+GFCCVYF+F+A N
Sbjct: 138 RRFQQPSLDFSEVAYCSFESGPLG-LRRYSMLARRIVTTFLFITQIGFCCVYFLFVALNI 196

Query: 167 KQVIEAANGTTNNCHNETVLTPTMDSR L YMLSFLPFLVLLV FIRNL RALSIFSLLANI 226
K V++ H + M ++Y+L L ++LL +RN L+ SL-A +
Sbjct: 197 KDVM-----HYYK-----MPVQIYLLIMLGPMLLNLVRNLKYLTPVSLVAAL 240

Query: 227 TMLVSLVMIYQFIVQRIPDPSPHLPLVAPWKTYPLFFGT AIFS FEGIGMVLPLENKMDPR 286
+ L + + +++ +PD + VA W T PL+FGTAI++FEGIG+VLPLEN M+ P
Sbjct: 241 LTVAGLAITFSYMLVLDPLDVHTVKPVATWATLPLYFGTAIYAFEGIGVVLPLENNMRTPE 300

Query: 287 KF---PLILYLGMI VITI LYISLGCLGYLQFGGANIQGSITLNLP-NCWL YQS VKL LYSIG 342
F + L GMVIV LY ++G GYL+ +G + +GSITLNLP L Q V++ ++
Sbjct: 301 DFGGTTGVNTGMIVIACLYTAVGFFGKYGEHVEGSITLNLPQGDTLSQLVRISMAVA 360

Query: 343 IFFTYALQFYVPAEIIIPFF----VSRAPEHCELVV DFLV FRTV LVCLTCILALI PRD 397
IF +Y LQFYVP I+ PF +RA + V +R VLV T +LA IP L
Sbjct: 361 IFLSLTLQFYV PVNIVEPFVRS HFDTTAKDLSATV----LRVVLVTFTFLLATCIPNLG 416

Query: 398 LVISL VGSVSSS ALALIIPPLLEVTTF YSEGMSPLT--IFKD ALISI LGFVG FVVG TYEA 455
+ISLVG+VSSS ALALI PP++EV TFY+ G + +KD LI I G GFV GT+ +
Sbjct: 417 SII SLVG A VSSS ALAI TAPPIIEVITFY NVG YGRF NWMLW KDV LILIF GLCGF VFGTWAS 476

Query: 456 LYELI 460
L +++
Sbjct: 477 LAQIL 481 (SEQ ID NO:4)

>CRA|89000000199481 /altid=gi|7297403 /def=gb|AAF52662.1| (AE003621)
CG13384 gene product [alt 2] [prosophila melanogaster]
/org=Drosophila melanogaster /taxon=7227 /dataset=nraa
/length=482
Length = 482

Score = 330 bits (837), Expect = 2e-89
Identities = 184/425 (43%), Positives = 262/425 (61%), Gaps = 32/425 (7%)

Query: 47 TTWFQTLIHLLKGNI GTGLLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFC 106
T+ F TL+HLLKGNI GTG+L +P A KNAG+ +G +I+G + HCM +LV C+H C
Sbjct: 74 TSNFDTLVHLLKGNI GTGILAMPDAFKNAGLYVGLFGTMIMGAICTHCMHMLVNCSEL 133

Query: 107 RRLNKSFVDYGD TVMYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCCVYFVFLADNF 166
RR + +D+ + ES P LR ++ RR+V FL +TQ+GFCCVYF+F+A N
Sbjct: 134 RRFQQPSLDFSEVAYCSFESGPLG-LRRYSMLARRIVTTFLFITQIGFCCVYFLFVALNI 192

Query: 167 KQVIEAANGTTNNCHNETVLTPTMDSR L YMLSFLPFLVLLV FIRNL RALSIFSLLANI 226
K V++ H + M ++Y+L L ++LL +RN L+ SL-A +
Sbjct: 193 KDVM-----HYYK-----MPVQIYLLIMLGPMLLNLVRNLKYLTPVSLVAAL 236

Query: 227 TMLVSLVMIYQFIVQRIPDPSPHLPLVAPWKTYPLFFGT AIFS FEGIGMVLPLENKMDPR 286
+ L + + +++ +PD + VA W T PL+FGTAI++FEGIG+VLPLEN M+ P
Sbjct: 237 LTVAGLAITFSYMLVLDPLDVHTVKPVATWATLPLYFGTAIYAFEGIGVVLPLENNMRTPE 296

FIGURE 2C

Query: 287 KF---PLILYLGIVTILYISLGLGYLQFGGANIQGSITLNLP-NCWLYQSVKLLYSIG 342
F +L GMIV LY ++G GYL++G +++GSITLNLP L Q V++ ++
Sbjct: 297 DFGGGTGVNLNTGMIVACLYTAVGFFGKLYGEHVEGSITLNLPQGDTLSQLVRISMAVA 356

Query: 343 IFFTYALQFYVPAEIIIPFF----VSRAPEHCELVVDLFVRTVLVCLTCILAILIPRLD 397
IF +Y LQFYVP I+ PF +RA + V +R VLV T +LA IP L
Sbjct: 357 IFLSYTLQFYVPVNIVEPFVRSHFDTAKDLSATV---LRVVLVTFTFLLATCIPNLG 412

Query: 398 LVISLGVSSSALALIIPPLLEVTTFYSEGMSPLT--IFKDALISILGFVGFVVGTYEA 455
+ISLVG+VSSSALALI PP++EV TFY+ G ++KD LI I G GFV GT+ +
Sbjct: 413 SIISLGVAVSSSALALIAPPPIEVITFYNVGYGRFNWMLWKDVLLILIFGLCGFVFGTWAS 472

Query: 456 LYELI 460
L +++
Sbjct: 473 LAQIL 477 (SEQ ID NO:5)

>CRA|18000005127815 /altid=gi|7509795 /def=pir|T26845 hypothetical
protein Y43F4B.7 - Caenorhabditis elegans
/org=Caenorhabditis elegans /taxon=6239 /dataset=nraa
/length=607
Length = 607

Score = 258 bits (652), Expect = 1e-67
Identities = 142/418 (33%), Positives = 235/418 (55%), Gaps = 19/418 (4%)

Query: 40 RFGQSNSTTWFQTLIHLKGNI GTGLLGPLAVKNAGIVMGPISLIIIGIVAVHCMGILV 99
R NS T Q IH++K +GTGLL LPLA K++G +G I ++I ++ ++CM +V
Sbjct: 42 RLPTENSLTPEQAFIHMVKAMLTGSSLPLAFKHSGFLGLLITVLCICLICLYCMRQVV 101

Query: 100 KCAHHFCRRNKSFDYGDVYMGLESSPCSWRNHAWGRRRVDFFLIVTQLGFCCVF 159
AH C R + +DY + + +E P W++ + ++ ++V+ + ++QLGFCCVF
Sbjct: 102 FAAHFVCNRNRGLIDYANIMRGAVEMGP-PWIKRNGYFFKQLVNVNMFISQLGFCCVF 160

Query: 160 VFLADNFKQVIEANGTTNNCHNETVILTPMDRSRLYMLSFLPFLVLLFIRNRLALSI 219
VF+ADN + NN T I + + +ML L + + + IR L L +
Sbjct: 161 VFMADNLDFF-----NNNTSI--HLSKAVWMLLLLIPMLSICSRRLSILAP 206

Query: 220 FSLLANITMLVSLVMYQFIVQRIPDPSSHLPVAPWKTYPLFFGTAIFSFEIGMVLPLE 279
F++ AN+ +V++ ++ F + + S LP PLFFGT +F+FEG+ +++P+E
Sbjct: 207 FAMAANVVVVAVAVVLLFFLSDLRPISSLWFGKATDPLFFGTVMFAFEGVAVIMPIE 266

Query: 280 NNMKDPDKFPL---ILYLGIVTILYISLGLGYLQFGGANIQGSITLNLPNCWLYQSVK 336
N+M+ P F +L ++V ++ G GYL G +++ + TLNL P YQ++K
Sbjct: 267 NRMQSPHAFISWNGVLNSSCLVLAIFSVTGFYGYLSLGNNDVKDTATLNLPMTPFYQTIK 326

Query: 337 LLYSIGFFTYALQFYVPAEIIIPFFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRL 396
L++ I +Y LQFYVP E I + + P + + R V LTC +A LIP L
Sbjct: 327 LMFVACIMISYPLQFYVPMERIKEWTRKIPVDKQTLYIYARIYSGVILTCAIELIPHL 386

Query: 397 DLVISLGVSSSALALIIPPLLEVTTFYSEG-MSPLTIFKDALISILGFVGFVVGTY 455
L ISL+G+ S ++AL+ PP +E+ T Y++ +S K+ ++ F+GF GTY
Sbjct: 387 ALFISLIGAFSGASMALLFPPIEELLTSYAKNELSTGLWIKNIVLTFAGFTTGTY 444 (SEQ
ID NO:6)

>CRA|335001101719045 /dataset=FastAlert /length=476
/altid=Derwent|w0200071709.21
Length = 476
Score = 909 bits (2324), Expect = 0.0
Identities = 450/476 (94%), Positives = 459/476 (95%)
Frame = +3

Query: 108 MSTQRLRNEDYHDYSSSTDVSPEESPSEGNNLSSPGSYQRFGQSNSTTFQTLIHLKG 287
MSTQRLRNEDYHDYSSSTDVSPEESPSEGNNLSSPGSYQRFGQSNSTTFQTLIHLKG
Sbjct: 1 MSTQRLRNEDYHDYSSSTDVSPEESPSEGNNLSSPGSYQRFGQSNSTTFQTLIHLKG 60

FIGURE 2D

Docket No.: CL001062CON
 Serial No.: TO BE ASSIGNED
 Inventors: WEI, Ming-Hui et al.
 Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

Query: 288 IGTGLLGPLAVKNAGIVMGPISLLIIIGIVAHCMGILVKCAHHFCRRLNKSFVDYGDTV 467
 Sbjct: 61 IGTGLLGPLAVKNAGIVMGPISLLIIIGIVAHCMGILVKCAHHFCRRLNKSFVDYGDTV 120

Query: 468 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCCVYFVFLADNFQVIEAANGTTNNC 647
 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCCVYFVFLADNFQVIEAANGTTNNC
 Sbjct: 121 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCCVYFVFLADNFQVIEAANGTTNNC 180

Query: 648 HNNETVILTPMDSRYLMSFLPFLVLLVFIRNLRLALSIFSLLANITMLVSLVMIYQFIV 827
 HNNETVILTPMDSRYLMSFLPFLVLLVFIRNLRLALSIFSLLANITMLVSLVMIYQFIV
 Sbjct: 181 HNNETVILTPMDSRYLMSFLPFLVLLVFIRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Query: 828 QRIPDPSHLPLVAPWKTYPLFFGTIAFSFEGIGMVLPLENKMKDPRKFPLILYLGMIWT 1007
 QRIPDPSHLPLVAPWKTYPLFFGTIAFSFEGIGMVLPLENKMKDPRKFPLILYLGMIWT
 Sbjct: 241 QRIPDPSHLPLVAPWKTYPLFFGTIAFSFEGIGMVLPLENKMKDPRKFPLILYLGMIWT 300

Query: 1008 ILYISLGCLGYLQFGGANIQGSITLNLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIP 1187
 ILYISLGCLGYLQFGGANIQGSITLNLPNCWLYQSV+LLY GI TY LQFYV A+II+P
 Sbjct: 301 ILYISLGCLGYLQFGGANIQGSITLNLPNCWLYQSVELLYLGGICLTYPLQFYVSAKIIVP 360

Query: 1188 FFVSRAPEHCELVVDLFVRTVLVCLTCILAILIPRDLVISLGVSSSALALIIPPLLE 1367
 VS + C L+VDL + + ++C TCILAILIPRDLVISLGVSSSALALIIPPLLE
 Sbjct: 361 VIVSWVKCCTLMDLGIGSAMLCCKTCILAILIPRDLVISLGVSSSALALIIPPLLE 420

Query: 1368 VTTFYSEGMSPLTIFKDALISILGFVGTVVGTYEALYELIQPSNAPIFINSTCAFI 1535
 VTTFYSEGMSPLTIFKDALISILGFVGTVVGTYEALYELIQPSNAPIFINSTCAFI
 Sbjct: 421 VTTFYSEGMSPLTIFKDALISILGFVGTVVGTYEALYELIQPSNAPIFINSTCAFI 476 (SEQ ID NO:7)

Hmmер search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	223.3	3.5e-63	1
PF01091	PTN/MK heparin-binding protein family	2.0	9.5	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01091	1/1	192	208	..	1	17	[.] 2.0 9.5
PF01490	1/1	71	451	..	1	467	[.] 223.3 3.5e-63

FIGURE 2E

1 AAAACCAGAA AGTCAGATAG TCCCTGTCTC ATCTTCAATC TCTTTATTG
51 TTATTTAGTCT GTTCAGGCTT TCCATTCTC CCGTATTCA ATCTTGTTAG
101 GTTGTATTT TCTAGGGATT TCTCCATTTC ATCTGGGTTA TCCAATATGT
151 TGGCAAATAA TTGTCACAA TAGCCCCATA TGATTCTTT TATTTCTGAA
201 GCTTCTGTG TAGTGTCTC ACTTTCATTT TTATTTTAT TAGCTTCTT
251 TTTTTCTTA GACTAGAAA GGGTACGTCA ATTAAATT TTCCAAAAAAA
301 TCAACTCTAG TTGTTATTGAT TTGTCGTGTT TTTTTCTG TTGTCATTT
351 GATTTATTCG TGTTCTGCTC TTCTTCTTCT TCTTTAACT TTGGGTCTT
401 TGAGCTCTC TTTTCCAGT TTCTCTGAGGT ATAATGTTAA ACTATTTAAT
451 AGGTCCTTT CTTCCTCTT AATGTAGGCA TTATGTCCTA TAAACCTCTC
501 TCTTGAACCT ACCTTGTGCTG CATTCCATAA GCCTTGGTAT GTTATGTCCTC
551 CATAGGCAAT TGTCGAAAAA TATTTTTAA ATTCCCGTT TGATTCATC
601 TTTGACCCAC TGTTGTITC GAAGCATAGG ACTGGGTATG GTGGCTCAC
651 CCTATAATCT CGAACCTTG GGAGGCCGAG GTGGGCAGAT CACCTGAGGT
701 CAGGAGTTG AGACGCCCTG ACCAACATGG TGAACCTCGT CTCTACTAAA
751 AATACAAAAT TAGTCGCGC TGTTGGCAGG TGCTCTGTAAT CCCAGCTACT
801 TGGGAGGCTG AGACAGGAGA ATCGCTTGA TCCAGGAGGC AGAGGTTGCA
851 GTGAGGCAAG ATTGCAACAC TGCACTCCAG ATGGGGCAAT AAGAGCGCAA
901 CTTTGTCTCA AAGAAAAAAA AAAGCGTGTG TTAAATTTC CACATATTG
951 TGAAATTCTC AAGATTTCTC CTGTCATTGA TTCTAGCTT CATATTATTA
1001 TGTTCTGAAA GAATATTAAAT ATGATTTCAA TCTTCTTAA TTAAGGCTT
1051 GTTTTCTGGA CTAGCATATG GTCTATTCTA GAGAATGTTT CAAGTGTGTT
1101 AGAGAAAAAA TGTTGATTCT GTTCTGTGTT AATGGAAAGT TCTGTATATA
1151 TCTGTTAGT CTATTTGGTT TAAAGTCGA TCAAGTTCAT TTATTCCTT
1201 ATTTCTCTC TAGTTGCTCT ATCCATTGTT GAAAGTGGGA TATTGACCT
1251 CCTACTATG TGTTGCTATC TATTCTCCC TTCTAGGCCA TTAATATTAG
1301 TTGTTGTTGTT TTAGGTGCTC CAATTTCGA TGCAATATA TTTACAGTTG
1351 TGTCTTCTG ATGAATTGAC CCCTTTATTA TAAACAAATG ATCTTCTCTG
1401 TCTCTTGTGA CAGTTTTGAC CTGAAGGCTT ATTGTGTCAT TAATTTGTTAA
1451 AAGAAAAGTC TGAACAAGG AGGTAAAGG AGAACGCTAG ATAATACAAT
1501 ACTGAAATGT TGCCATCCAT TTAAAGATGT TACTTTAAA ATTGAAATGT
1551 ATTAAGAATG ATGTTGCCCC TACCCACAG TTCCATTCCG AGTAGCAACC
1601 ACAGATGATA GTTTGTTGAT GCTTCTGAAA AATTGGAAAGT TTTAAAATA
1651 TGATATTTC TTATTTAAAG AGCAATACA ACTCATCGG ATGTTGAAAA
1701 GAAAATACAG CGAGTGTAAA ATTAGCAAT ATTTCACAAA CCCACAATC
1751 AAGGGACAGT GCTCTTCGAC TGACTCTGC CCCATGCCA AGATCAATGC
1801 CCTGTTGAGT TCTCTTGCAG AGTCCCCAGG GCCCAGGAAC ATAGTCTTC
1851 CAGCAGTGGC AGTAATAGGT CGCCAGTGG TGCTGTGGAG CAGAGCTCCG
1901 GAGCTCAGTG AGAAAAAAAG CGCGGGCGCT CAAGGGAGCA CGTGACCTCG
1951 GCCTCTGGCG TGGGGCTGG GATCACGTGA TGAGGTCGG AAGCGGCTGC
2001 CGGGCAGCAA AGGAGGATGG CGAGGGCTGT ATACTGAACCG CGGGAAGGGT
2051 GGGCTGTGCT GAAGCCAGAG CGGGAGCCGG AGCTGGGCC AGAACCCGAG
2101 CAGTGAAGT CTCCACTGAC GAGTTCCGG TGCGGGCGCT CGCCGCCCTG
2151 GGCAGGACCC ACCTCGCTT CTCCTCCGGC TGCGAGATCG TCCAGGTAG
2201 GCACTGGATC CGCCGGGGCT GTGGGTCCGC GACTCCTTGG CGTCCCCGGG
2251 CGGCACTGCG GGTCAGCGC TGACACCCCT CTGTAATTG GCGGAAGCGT
2301 GGAGATCCCT TGTCCCTCGC GTATCTCCCG TTGACTCTGT GGGGTTGGGA
2351 TCTCACCGTC CTGTTGACT GACAGGTGGG GGAAACTGGG GTAGATGGTG
2401 AAAGTAACCC AAAGGACCAT CTAGGGCTC TTTCACGCTT CGCACAGTC
2451 TCCCCCTTC CAGCAAATG CTGGCCCGT GCGGGAGCG TGCTTGGAC
2501 AGGCTATAA TGGGCTTTG GGTCAAGAAC GCAAGGACGC TGGGAAGTCG
2551 TCTGTTGTCG CTCCCTCCG GGACAGTTGG AGAAAATGAG CCCTTACTCC
2601 GGGAAAGGGT AAGGGCTTGC CTAAGGTCAT CCAGTGGATT AATCGGAGAC
2651 CGGAGACCT GCGACTAGAA TGCAAATGTT CCTAACGCTC AGCAGCTGTT
2701 TGCTTTCTC CACACCCGCT CTCGGGGAA ACTTCACCTG TGAAAAGGC
2751 CTCTCTCTG TCCCCCTCTC TTCTAGCTCT CTCCCCCTTT AGCTGTCTG
2801 ATTTCCACC GCTGGGGTTG GATTTGCTCT GGGTGTGGTT CCCTGTTTG
2851 TCATTATTTT TCTGCAAATT CATCCTCTG TAGGTTGGT TTCTAACCTT
2901 CCTGCATTCT ATGTAAGTC CACCAAAAATG TAAATATGA ATCGGAATGT
2951 GCTTCTGGG AGATAGGTGG CTGAGCCAG GTTGTGGAGA GCCCTGACGT
3001 TAACTTGAAG AATGAAAAGA CCTTTGCTT ATTTCCTG TAACCTGTC
3051 GATTTGGGAT TGCTTATTGAT GATGGACGT TTGCAAGTTT TTGAATTGG
3101 CTGAAGATAG CATCATGGT CAATGGACAG AACAGAGATT GGGGAATCAG
3151 GATTTTTGT CCTAGCTCTG CGCGTTACCT GGCACCTTA AGTGAATCGC
3201 GTTGGGTTT CTCACTGCTAG ACAGTGTGTT AATGGAATT TAAAGGGCC
3251 CTTCTGCTG GATCTGGATG TTGTCATCT TTCTAGGGTT GTTTTTTGT
3301 TTGTTGGTTT TAAATAGAG ATGAGGTCTC ACTATGCTGC CGAGGCTGAT
3351 CTCAAACTCC TGGGCTCAAG TGATCTCCCC ACCTTGGCC CCCAAAGAT

FIGURE 3A

3401 TGGGATTACA GGGGTGTGAG CCAGTCCCC TGACCAGGGT CTGTTTGTTT
3451 TTTTATTCCG AGAGTTTTA CCGCTGTG ACACTGAGTA TCAGCCTTC
3501 AACAAAGCTT AATCTAATTG TGAGGAAGC AGTTTCTCT GCTTATTCT
3551 CTGTTGCTAT AAAATCTCC TCCCTTCT TCCTATCTCT GTATTATGTC
3601 TAAGCTAAAT ACTAACAGCT GAAAATGATT TTAAACTGTC TGTTATTATT
3651 TTAAACATGA TCAGGGCCCT CTCTGACTC TTGCTAGAG CCTCGTTAC
3701 AGTAATTAAAC TTACTGTAC ATTAAAGACA TGTTTGTG AAAAATGTT
3751 TTGAAGTCAA GTGAAAAGGG ACAAACTTGTG TGTTTGCTG GGGATGGAGG
3801 CTACGTGCAAG CAGAGGCTGTG GCTGATAACA GCTTAAAGCC TCTCCCTTG
3851 TTTCTGATT GTATCGTTA TATTGCGCTG CTCTGGACTC CTTGTTTCC
3901 CTTAAAGGCA TGAGCTGTT CATTCAAGTG CTCCTTGAG CAGTCGAAG
3951 TGCTCAGAGT TTCTCTGTT CAAAGGCAG TGTAAGAAAA AGGATTCCAT
4001 TTATTTATA ATATTCTGGA GACTACAAC GGGACCAATA GATGAAAGTG
4051 CCATAAGGGA AGGGTGTG TGAAAGTGT AAAACCTTCA AAGAATTAGT
4101 GGTCTCTGT ATTAGAACAC TGAGCACGGG GCTCCCTGTC ATGGAGGTA
4151 ATCGTCTGTG GGCATAACT TCAGGGATGT TGAGATGAA ATTAGATTGT
4201 TGGGTAGAGG GTTGGACTAG ACAAAATTT AAGTTTCTT TCAACTCAAG
4251 AGTCTGTGAC ATTCTAGGAC TGGAACCTACT AGCATGTAGA GTGGATGGAG
4301 CAGATGTC CAATTAGCA TGTTGGATGG ATGGAGCAGA TGCCACTTA
4351 TTACTAGCAT GTGGATGGAA TGAGCAGGT GTCCACTTAG TGCCATGTAG
4401 AGTGGATGGA GCAGATGTC GCTTACTAGC ATGTTGGATG AATGGAGCC
4451 ATGTCACCTT ATGCGATGT AGAGTGGATG GAGCAGATGT CCACTTATTA
4501 GCATGTGGGA TGGATGGAGC CGATGTCAC TAGCACCTAG ATGGAACGG
4551 TGGAGCAGAT GTCCGCTTAC TAGCACCTAG ATGGAACGG GCAAGATGCC
4601 ACTTACTAGC ATGTTGGATG GATGGAGCTG ATGTCACCTT ACTAGCATGT
4651 GGGATGGATG GAGCTGATGT CCACCTACTA GATGTTGGGA TGACGGAGC
4701 CGGTCTTAC TTTACTAGCAT GTGGATGGAA CGGAGCGGT GTCCACTTAC
4751 TAGCATGTGG GATGGATGGG GCAGGTGTC ACCTTACTAGC ATGAGAGTG
4801 GATGGAGCAG ATGTCACCTT ACTAGCATGT AGAGTGGATG GAGCAGATGT
4851 CCACTACTA GCATGTGGGA TGGACGGAA TGTTGTCAC TTAACTAGCA
4901 TGTTGGATGG ATGGAGCGGA TGTCACCTA CTAGCATGT GGATGGATGG
4951 AGCAGATGTC CACTTACTG CATGAGT GATGGAGCT GATGTCAGT
5001 TTGTTGATTA CTTTGTCTT ATTATAAACCT TTGTCAGG TAACTATTCT
5051 CATATAAAGT ACTCTGCTT TTTCTTCTT TTATCACCA CCACCTCCCC
5101 TCCAGTGGAT ATTCCTGTT TTAAATGCT TGATATCGCT TCAAAGGTCA
5151 GATGAGTGAAG TACTCTCTG TTCTGCTTT TCCTGGCTG GTGCTGATAA
5201 CGCTTCCAA AGTGCATGAC TGATTAGCAT TACTCACCA CAGGGCAGT
5251 TTGCTTCTT TCCCATAGAG GAACCTCAC GGAATCCGTT TATTCATC
5301 CAGGCTTCT CTTGTTTCCC ATAGAAAGAG CTCTCACTGA GTCTGTTAC
5351 TTCCACCCAG GCCTGGAGA AATCTGTCAC CTCTCTCTT TGGCCAGGCC
5401 TTACTGTGAT GAGCACATAA AGGTAGCTTC TACTTAATGG GCATGGGGC
5451 CGATGGATGG GGCATTGTAAG ATAGGCTGAA ATAGGAACCA CACGGTGTG
5501 CATTGGGGT TGTCTCTT TTATTCCCC AAAATATTTC TCTTGGAAAGC
5551 CTGGACACCE AGGGCAGTT CTTTTTACAT TTATTATTA TTTTATTATA
5601 TTATTATTAT TTTTTGGAG ATGAGGTCTC ACTATTGTT CCACGGTGGT
5651 CTTGAACCTC TGAGCTCAAG CAGTCCTCCC ACCTTGGCCCT CCCAAAGTGC
5701 CGGGATTACA GATGTGAGG ACCATGCTTG GCCCCAGGGC TAGCTTAA
5751 TGACCATCTC TAGTAGGAAA AGCCACTCTG TGTTTCTCTT TTCCATGAAG
5801 TTAGGAAATC TGTCTGTGG TTACTGAGAT GTTCATGTCA CTTAGATCAC
5851 CATCTCCAAG GTAGGGACCT GGCTTCACAA TCCAGGGTT TAAATGGAGC
5901 CCATACTGCA GACTTTGTT AGTGAACCTT CTCACTTCT GTCTTGAAC
5951 TTCTCTGTAG TAATAATCAC AATTGCTATC ATTAAATGAGG GTTATTATG
6001 TTCCAGGATCA CATATCTAAC ATTATTTATC TTCTTCTCTC TATCTCATA
6051 ACAATATTGT GATGTAGATG TTATAATGA CATCTTCAG ATGAGGGAGC
6101 TGTGCGAAAG GGAGATGAAT TAACTGTCTC AGAGTCACAC TACCAACTG
6151 CAAACTAGG TGCTTTTAT TGTCAGGAAAT ACCCGCTGCA GACCTATCC
6201 TGCCCCAGGC TCTGGGGCA GCTTGTTCG CAGGGAGATT TTAAGGAGGG
6251 TATATAATTG AAAGGTGTGT AGAAAAGATA CTGGACTGGG ATGCTGGTT
6301 GCTGGACTGT CATCTCAAT CTTTGATTCT ACTCATCTG GGGCTGGAT
6351 GAGTCAGCTC TTGTTGTGG GCCCTGGTT TCTGACCCCT AAGAAGGAAG
6401 CTGGAGCTT ACCTTCTCA AAGCTTACAC TGCCCTAAC ATTAGTGAT
6451 CTTCATGGTGGGGAGAAAA TGTCGGTGTG TTGCTGTGTC AGCAGCTGCT
6501 TTGTCAGGAA CCTGCTGAGG TCAGCAGCTG CCCCCTGAGT GTTCTAGCAT
6551 CAGACTCTA CAGGAAAAAG TCTCAATT TGGAATGTTC TGCTCTGGTA
6601 AGTGGATGG AATTCTATCT GATGCTGTTT TAAAACAAA TTATGTAGAA
6651 GCAAAACCAT TTTACTTCCC TCACTGTAGA CCACACATAG CAAACAGCT
6701 TGTCCTTGTG TTTCATGTTT TAGAATTCCA TCGACAGAGA GGAGAAAATA
6751 CATCTGGGGAA ATTTCGGCT GCTCTGAGTT CCAAACTTCA AACCAATGTA

FIGURE 3B

6801 ATTGTTTCAG AATAACGGAT GACACTTTA GCTTGAAAC AAGGGCGCC
6801 AATGGGTGAA TTCTGGTGG AGGTGAGGC TAGGGTGTAC CTATCATAAT
6901 AGATCATAT ATTTTTGTA GTGTTTATA TAAATCTACC TATAATCAAG
6951 ATTACCTTAGG AAGCTAGTT AAAATAAAC GCCTCTTGC TGTAAATCCA
7001 TCACCTTGAG AGGCTGAGAC AGGTGGATCC CTTGAGGTCA AGAGTTGAG
7051 ACCAGCCTGG CCAAACCGA GAAAATCCAT CTCTACTAAA AACACAAAAA
7101 ATTATCTGGG CATGGTGTG GACGCCGTTA ATCCCAGGCC CTCGGAGGC
7151 TGAGGGCAGG GAATCGTTG AACCCAGGAG GCGGAGGTTG CAGTGAGCA
7201 AGATCACACC ATTGCACTCC AGCCTGGCA ACAGAGGGAG ACACCATCTC
7251 AAAAAAAA AAAAGAGACA AAAAGACAA AACAACAACA AAAAAACATA
7301 GGCTGGCATC GTGACTCAT CCCTGTAATC CCAGCACTTT GGGAGGCCA
7351 GGTGGGTGGA CCACCTGGT CAAAGAGTTT GACACAGGC TGCCAAACAT
7401 GATGAAACCC CGTCTACT AAAAATAGAA AAAAATTAGC CAGTTGTGTT
7451 GGCAGCATGTC CGTAACTCCA GCTACTCGGG AGGCTAAGAC AGGAGATTG
7501 CTTGAACCTG GGAGGGCAGG GTTGACCGA GCCAAAGATCG CACCACTGCA
7551 CTCCAGCCTG GGCAACAAGA ATGAAACTCC ATCTCCAGTA AATAAATTAA
7601 AATAAATAAA TAAAATAAA TAAATTTAA TGCTAAGGTG GAATCAAGTT
7651 GGGCCGAGA ATTATTTT TTTTCTTGTG CAGTATGTTT CATTAAACCC
7701 AATATATCCC AGATATTAC ATGGCAATAT ATAATCAGTA TAAAGATTAT
7751 TAATTCATGG GATATTCAC AATTTTTTG TTACCAAGTT ATTGAATATC
7801 AGTGTGACA TTCATTTT ACCAAAGTGT ATTCAGTGT TAAGATAGCT
7851 ATTTATGGCT AGTGGTTACT GTACTGGAT GTACAACCTT AGAATATGTT
7901 ACCATCTATT GATCTTAATC TCCTTTTATT TTGAACAAAC CCAGTCACTA
7951 AAAAAATGAA ATTGGAACTC TGAAACCTTA GAAGTGAAG TGACTTGA
8001 AATCATCTAA TGCACTTTG TCAAACTTAT ATCAAAATAG GAAAACAACT
8051 TTGGGATTAG AATGACAGCC AGATTATGTT CTCTGAGTC CTGAATCCA
8101 TGCTGTTAAA ATGGGAACAT TAGCATTGA ATTATTAGA AAAATTCTG
8151 GCCTTGCCTT AAAAAAAA AATCACTGTG TAATTCCTT TAAATTTG
8201 CACTCTGAA AAATTTAAC CCTACAATT TTATTTTA AAAATAGAAT
8251 AAAATTTATT TTATTTTAA AAATAAAAAT TCAGTTGCA CATACTTTT
8301 CCATATTGCA TCCGTTGCA AAAGTGTGTC CACCTGCTCA TTTTTAGTGC
8351 CCATCTAAA ATGGCATATT TTGTAGATTG AAGAGCAACA TTGTCTATT
8401 TATACAGCTA AAAACAATAGT TACATAAGGA AAAAAAAGGA ATGTTTAAG
8451 GTTTGTACAC TTAAATTTT TTTTTTTTTT GGCATCAAC
8501 TTGCAAGCTT TTTTACTCA GTTGTCACT CTCTGAGTC TAAATATCTA
8551 ATGGAGATTG GGACTTTGTG TTCTGTTAT GTCTCTAGT AATCTGAAGG
8601 ACAAGCTTC CTTCAACTC CACATAGTAC AACCCCTATT TAGACAGTTA
8651 ACAGGTTACTA TTTAAATCTC CCATAGGGG GGAACGTGCA ATTGAGCAA
8701 TAGACTTGGC TATCAGATT CATCAAAGGG AGCCTAAGGG CAGTGTGCC
8751 ATGGATGCCA GCACTCATGG GGACAGACAG AGAGCAGGAG GAGGAGGCC
8801 TGTTTCCCA AAAGAGCCAT AGAAAGAACCT CGGGGGAGTG GCTCTGCCA
8851 CTGCTGTGTC TTGAACTCT TACATAACTG CTCTGAGAAA GGGCTTTGC
8901 TTGGATTTC TCAAGGATAA GGGAAACAGGC TTCTCCCGAG AGTGATCTGT
8951 TCTATTGGG AAGCATCTG CTTTGATAGA AAGTTCTTC TTACACCTAG
9001 CAAAAATCA GCCCCCTTGA CTCTCCACGT ACTGATCTA GCCCTGCCG
9051 ACCTTTGAG CCCAAATAAA CAAGCTTAAT CCATGTGACA GCTTTTTT
9101 TTTTTTTTTT TTGAGACGGA GTCTCGCTT GTGCCCCAGG CTGAGTGC
9151 GTGGCGCGAT CTCGGCTCAC TGCAAGCTCC GCCTCCCGGG TTACACCAT
9201 TCTCTGCCT CAGCTCCCG AGTAGCTGG ACTACAGGGG CCCGCTACCA
9251 CGGGCGCTA ATTGTTGTA TTTTGTAGTG AGACGGCTTT TAAAGACAGT
9301 TTTTGACCC CTCAGTTGC TAGGTGGAAC CTTCTCAGTG CTTTCAACCA
9351 TTCTCATTG AGTGGTTTC CTACCCCTCT TGATCCTAGT TCTGACCCCT
9401 GGATATACCA CAATTGTC TAATCCCCCT TATAGCATGC TGCTGGAAAG
9451 AGAACACATT ATCTGGCAAT TCTGAGTTGT GTAAACATGTA CCCATGTGTA
9501 ACATCTAGCA TGAGAGTGG ATGGAGCAGA TGTCACCTTA CTGGCTGT
9551 GAGTGGATGG AGCCGAGGTG CACTTACTAG CATGTGGGAT GGATGGAGCC
9601 GATGCTTACCATGATTCTC TCTGTCCTA ATGCAACCTA GAATTGTTGTT
9651 GGTTTATTG GCATCTTGG TTATTTTAC GCTTCTGTGTT GAGCTTATCA
9701 TCAACCGAAA CTCCCAAGCA GAATTTTTT TTCTGTGTT CAATATGCAT
9751 GCAGTTGCTT AGCCACATCT TCCATATCCC GCAGGCTTAT TGGACCTTAA
9801 ATCTATAGAT TTCACTCTCT TGTTGAGAAG TTCTCTAGC AATATTCTGC
9851 TGTTGGTAAAC TTCAAGTTT ATACACAAACA TAAAGAAAGT TCTCTGAGT
9901 GTTTGAGATA AATTGAACAT CTGACCAAG TAGACAAACAG AGAGGTTCT
9951 CGGGTGTAG GGAAGGATTG GGCAATTAAAT AAGTCCCTGT ATTCCATCTC
10001 TTCACTCTCA GTAAATATAA GGTGTCACCC TAAAGGAAGA AGTTGAGACA
10051 CAAAATGCAA TTTTAAACAG TTAACTTGGAA CTGTTTAATT GAACCAAGTG
10101 AGGACAGCTG CCGGGGACAC ACTTCAGGAT TGCTGGGGG AGTGGCTCCT
10151 TCGGCCCTTG TTACACAGA TTCTTAAAGG CAAAGGCAA CAAGGAGGAG

FIGURE 3C

10201 ACTGATAACAA AGTGACTTGA CAGGAATTCT CATCAGTTA CAGAAATAGC
10251 ATGGATTATT AGTGGCTGT ACATTTGGG ACTATAGGT ATGAGTTATG
10301 ATGTCAGTG TTAGCATTT ATGACTTAGT GGTCAGTT AGTCTAGAAC
10351 CCACATAGCA AGTGGCTCA AGAGGTAATT ATTTAACTCA AGGGGGGAGT
10401 GACACATGC TGCTCTACA TTTTAGTCG TCTCTGGACC CGTAATTAA
10451 AGGGATTCTT CAGATAAAAA GTTCTTTT TTTCACAA GATTCACTTG
10501 GAAGGTTCTA TCTTCAGATG CTTTGGTTT GTTGAAGGG ACTAGAAATT
10551 GGCAGCTTT TCTTTTTTC AGTAGAGGCA GGGTCTCACT ATGGTCCCCA
10601 GGCTGGTCTT GAACCTCCGG CCCAACGTGA TCCTCCACCC TCAGCTCCC
10651 CAAATGCTGG GATTACAGGT GTGAGACACT GCACCTAGCT GCTGTTGCA
10701 TAAATATTA TAGTTCTATG CACCTAGAAT ATTAGTGTCA GAGGGAGTT
10751 AGAGATATT TAGTTCTATG CACCTAGCTT TTGACACATT AAAATGGTT
10801 CACAGGTAAT AAGCAAATG TTGACAGGG TAGGCTTGGC GCGTGGGCC
10851 CCTGAGATAC CTGTAACATG ATTACAGGC TTATACCTGT ATAGCAAGAG
10901 GTTAAATGCA TGGTATTAAAG ATACTTCAGA GATTTTTTT TTCTCCCGC
10951 CCTCTAGTGA GTTAAATTGC CCCAGAGCTG GTTGGCGTCC TTGAATTCT
11001 CTAGCTCATG AGTAATATGAA GCTCTCATG ATTTTACGG AAGTGGCTT
11051 GGCAATGAAG CTAGGCGAGG TCGTCTCTGG GATTTCCAGG TCCTTGCTG
11101 GCATTTGCC AGGTACTTCC TTGAGGATG AGCTGGGGG TCCCTCCAC
11151 ATTGCAATT TTGAGAGAAA ATGGCATCTC CCGTGGATCT CTCTGGTGC
11201 AGACTGGGT GTTCCAAAAG GAGTACCTCG GCACTGGACCC TAAGGAGAGC
11251 CTCGGCGGA GCACCATCTT CTGGCAGGGT GTGCTGGGTG TCAGGGCAGG
11301 GTGGAGGTGTG TTGGCAGCG TTGGAGGTCC TGTCTCTCT CAAGGTAGCT
11351 GAGATAGAGT CCGCAGGCTT AAGGTGGGCA TCCAGGCCA TGCGGAGGA
11401 CAGTCTGACG GGCAAGTGC TTGCGCAGCT TGCCAAGTGT CGGGAGGATT
11451 TTGTCATT TTTATATTAAG TGTACCTTTT TTTTGTCACT TGGTTCTTG
11501 AGAGCAGGAA GTTACCTTCTT TCACTGTGCT GTAATACTCT CTATAGCAA
11551 CTGGGACTCT GTAGATGGTG TGTTTCAAGA TTCTGACAGG GGTCAAGGAGA
11601 TAAACGTTTC TGTTGTTAC TACCTAGCTG TTGCAAGGGCA GGTACTTCA
11651 TCTTTAGCA TTGTTCTTCTT ATCTTAAAG TAAGGGCTT AGATGACCT
11701 GTAAAGGCTC ATTAGCAAT GGTCTCTAGG ATTCTAGGG CCTACATCCG
11751 TCCCCAAATG TGCTTCTTGT GTGTTATTTT AAGAAGCCCT TGCTCTTCT
11801 TTGTTGTAG TATTAATAGT ATTCTGTAGT AAATCCACCC AGGGGACACC
11851 ACTCTCACCA CCCCCTTCAAC ACATTTGAAAG GACATTTTT TCTCTCACCA
11901 TTTTAAATAT GAGCACATCT ATAAAAAATAA AAAGGAAGAA GAGTTGGGA
11951 TGGGAGATGT TGAGACGGG GCCAGGGTGA GCACCTTTCA GTTCTCTGG
12001 CCTCTCTGAG GCTGCTTCA GCTACCATTT CTCACTACTC AGGTTGGCAG
12051 CAAGAAGGA GTCCCCAGGT CAGGGTATAA GAGTTACTGG TGCCCTCCAG
12101 AGAGTATAGG ATCAGCTGTG GGTACACAGCA GAGAGAAAGA GAACGGCATG
12151 TGTGGCTCTG GGAGTTGGT GGAGTTTCAAG CAGAATTGGG TGATCCAGAG
12201 GGGATTTCTG TTTTCTTTTT TTGTTGTTG TGTTGTTT TTTTTTGG
12251 ATGGAGTTTC GCTCTGTG CCCAGGCTGG AGTGCATG TGCAATCTCG
12301 GCTCACACA ACCTCCGGCA CCGGTTTCA AGCGATTCTC TGCCCTCAGC
12351 CCTCCGGAGTA GCTGGGATTAA CAGGCATGCA CCACCCAGCC CGCTAAATT
12401 TGATTTTA GTAGAGACGG GTTCTCCA TGTTACTCG AGTGGTCTTG
12451 AACTCCGGGAC CTCAAGGTGAT CGGCCCGCT TGGCCTCCA AAGTGTCTGG
12501 TTGTCAGGGC TGAGCCACCA CACCCAGGG AGAGGAGATT TCTTGAGTGA
12551 AATGTTCTCT CTATTGAAGG CAGAGAAAAG AGATATAAGG ATGAGAAATA
12601 CCCAGATTTC CATCCCCCAAG AGAGCTTGA CATATATAGA TATACGTGTG
12651 TATATGTTAT AGCTGTATAA TATAGTAACA TACACCGTGT ATATACGTAT
12701 ATATATATAT ATATATATGG GTGATTATAT ATATATATAT ATACAGGAGC
12751 ACGATGGAAC TATTCGACAA GGTCCAAGAC ATTATCTCA AGAAGGAGTAG
12801 ATAATCTGAA CCTAAAGGAAT AGGGAATCGG GAATTCAGG AAGCACTTCT
12851 CTTTCATTTT CCCCCACTCC TCCCAAGGAG TGCCCTCACTT CTGCTTGT
12901 TAGCTGTACT CGGGAAAATT AAGAAATTAA TGAGTGTAGC ACCACGTATA
12951 CCAATGGGAA GGATGGGAGT CAGAAGTCA GTGAACCTAG CCCGCTCTG
13001 TGACTTTGC ACTTTCCAT TTCCCTTGT ACCAGGCACT TTCACTTA
13051 ATCCATAGTG GAGCTGTCA AGTGAGCAAC TCTGACAATG ACAGCTTCA
13101 CCCCCAGGGC CACCCAAAAT ATGGAGCTCA AGGCTCCAGC TGCAAGGAGT
13151 CTTAATGCTG GCCCTGTCTCC CCCAGCTGCC ATGTCACCGC AGAGACCTCG
13201 GAATGAAGAC TACCAAGCACT ACAGCTCAC CGACGTGAGC CCTGAGGAGA
13251 GCGCGTGGGA AGGCTCAAC AACCTCTCTT CCCGGGCTC CTACCAAGGC
13301 TTTGGTCAAAG GCAATAGCAC AACGTGAGTA GTGTTACCT TCTCCCTCTC
13351 TGGGGGGGAT TCGTGTCTCT AAGCCTCCCT TGAGTTATT TTTCCCCCA
13401 ATTTCATCAAG TCTCTCACTT TACAGATGAA GGTCAAGCTG GAAGAGATTG
13451 GGGCAAGTGCAG TGCGCTGAGA TTGCGCTCC TGGGCTGCGA CTCTCTAGGC
13501 AGTTTCTTAC TCTTTTCTC TTTCAGCTGT GTTGGCCCCA CAAGGCTGGT
13551 GCGCAAGTGAAG ACCTTGAGAT TAAAAAAAGC TTCTACAGAG GACATTCTT

FIGURE 3D

13601 TAATTTAAAA GTGTGTCATC TGTGCTAGAA CCCAAATAA TTTCCAAGCA
13651 TAATCGGAAG CTTCTTTCG AAAGTCTCCC CCCGAATTCT GCCCCATCAC
13701 CAAATCAGTA TTCACTTGAC TGAAGAACGTG GGAAGAGAGA AGAATTAAC
13751 TCTGCACTTA AAAATTCAAG GTTGGTAGG AAAGGAAAGA TAGACTTTGC
13801 ATTCCTCAAAG GAGGGCTTAA TCTCTTGTCT CCAGAAAATG GGACCCAGA
13851 CTCATTTGGG CTGAGTTGG CCCGCTTCAG GTCTCACTTT CCCAAATGT
13901 AAAGAAAAAT TGAGGACTCC ACCACAAAGC TATGCTGGCT GTGTTGGCT
13951 CACCACTTG ATTAGAACAT TGAGGAAAG TTTGCTACT CCATTGAGTT
14001 AGTTTCCCAG CTACTCCGTA TTTCAGCAGA CCTCTGACTT TTCTCTGTGT
14051 CCCAGCATCT CAGCTTTGC AGTCCTGTTT ATTCCCTCAAG CTAGCTATT
14101 CTCCTTCTG TGTTTTCTG TGGAAGTGTG GTGACTTAAC GAGAGATCCT
14151 TCATGCTCA GACTTATGCC ATTCCCTGATG ACTGCCAAG CGGACCATGG
14201 AAGCTCTGG GCTCATCACT GGAGAACGTC CCTCTGCCGT CACTGTCCTG
14251 TGGTACAGGG CATTTTCTC TGGGAACTGG GGTGGAACTA GAAGAATGTC
14301 TGTCACATT CCTGGCCCGT CACCAACACT AGCTGATTT TATGCCCTAG
14351 GCTGGAAGTA CTCAACCACT CTCCTAAAGAT TCTGTTCTG TAGCTTATT
14401 CTCGGGGTA TGCTTTGTA GATTTCCCTAG TGGCTGCAAG TGGGAGTTAG
14451 CTGGTGTAG ATTGCTTAGA GCACAGCTGG CAGCACTGTG GATCACCTG
14501 CCCCTTTTC CTCCAACCTT ATCAGCATTG GCAGCCCCA TGAGAACGA
14551 TCTCCACACA CAGGCAATGG CATGATGATCCTG CTTCCTTCA GAGGTCTG
14601 TTGTTATCGT AAGATACCTC TAAGCTTCTC TCTCTGTAAT TTCTCTGCA
14651 GTTTTGTCT CTTTTGATC TCAGATATCA ACTTGCTAA GCAATATTAA
14701 CGACAGTGGG TCTGGATTTT TATGTTTATA GAGACATCTC TGAAGCTCAA
14751 AACCTACAA CTCAGCAACTT TAGGATAGTA GCTCATAGGT TTTGGACAAA
14801 ATTATGCTCT TGTTCCTGG AAATCGAACAA AATCAGAACG TACCTTCCTC
14851 AGGGCTGTAT TGTGACATT TCCAGGGTAT ACTTGTCTC GAGTTTCCCT
14901 TCTGCTCTG ATGTTGTGAT ACAGCTGAGG TGACAGGGAA AGCCTATCTG
14951 TAGTTGATGG CAGGTATTAC AGTCCCCTCA CAGGTGGTAC AAGATAAAGT
15001 AATTGCTGG GCCTTGGAGG ACTGGTTGAG TACTTCCAGC CTGGGGCATA
15051 GGATCCACGC AAGGATTAT TATAGAAAACCA TGCCAGGTAT GATTAAGGTA
15101 GAGGGTGTATT TGGAGGACCT TCTAACCTA AATTAAATT TTAATATGTC
15151 GGAAGTGTAA GAGACAAGTT TTGAGCTGG GTTCCCTTTA TATTCTGGT
15201 TTGCCCCCACCT TTTTATCTA GTTGGCGCAA GGAAACAAAT ACATGGAAGT
15251 ACTTCTACAC CTACTGCACA TATGCTGCA CACACCTGGC TCTTCTAGCA
15301 AGTCACAGGG TCAGCAAAAAA CCCCCTAGTTA GGGGGTGCCTA ATAGGAACCC
15351 CAAACACTTC CATGAGTTTC ATGGGTTACT TCCTTTATT TTTTGGACAC
15401 AGGGCTTGC TCTGTTGTC AGGCTGGAGT GCACTGGCAC AATCATGGCT
15451 CACTGCACCC TCCATCTCCCT GGGCTCAAGT GATCCTCCCA CCTTAGTTTC
15501 CTAAGTAGCT GAGACTACAG GCATGCTCTC GGCCTACTTT TGTATTTTT
15551 TTTTTTTTT TGAGAGATA GGGTTTGCT ATGTTGCCA CTTAGTCTTA
15601 AAAGCCTGGG CTCAGTGT CCGGCTGCGT CGGCCTCCCA AAGTGTCTGG
15651 ATTATAGGCA TGAGCACCAT GCCTGACCTG TGAATTATT CTTAGTGTGT
15701 TCAGTGAGGT TATTTACTAA CACTTGATGT TACCAAGCTA TTGACTGCTT
15751 CGAAGACAGC CTCATTTTAT GCTGTTGGC AGATTTTCT TCTTGTGCC
15801 CCTCTGAGTT CTTATATATA TATCAAGCCT CCGTGCTTCTT CCCCCATGCA
15851 AACTGAAACG AGCAGACTGA AACTGGCTCT CTAAGGTGA GCTGGAGTAG
15901 TCATTGCAA AATGTGGTCT GCACACTTT TGGGCTTCCC AAGACCATT
15951 CAAGAAGTCT ATGAGGCTAA AACTCTCTT ATAATAATAC TAAGATGTTA
16001 TCTGCTTTT CACTTGTGGA TATTTGACT TATAATGTAG AAGCAATGTT
16051 GGGTAAAAATT AACTGTAGA AGCAATCAAG GCAGTGGCAC CAAATTATAC
16101 TAGTTGCTG TTGTTTTTC ATCGCCACAC ATGCCAAAG AAAAAAGCCC
16151 TTGCACTTA AGAATGTCTT TGATGAAACT GTAGGATTAC TAATATTAA
16201 AAATTTGAGA CCTTTCACTA TAGGCTTTTA ATATCTGTG TGGCAAATG
16251 GGAAGTATGC ATGAAGTACT TCTATGAGA CCAAATATG TTACTTGTCT
16301 TAAGGCAAAG ACCTCGAGT ATTATATGAG TTGCAACCA AACTTGTG
16351 CTTTTTTTTT TTTCATAGA ACTAGAACAG ACAACTAAC AACTGTAGT
16401 CATTCAAGACC CGAGTACTTG TAAGACATT TCTTGAAAT GAAAGAACATC
16451 AGCCCATCAC CTCAGGAAA ACAATAGATA ATACATATCT GTGCCCAAGA
16501 ATAAAATTCAGGCTTCAAG CAAAATTAAGG AAAAAAAACCC AACTTGTATC
16551 CAGTACCATG AGCTTGATAG CCCCTCTACT TGAAGACTT TCTGTAGG
16601 TTAGTGTGA TATTAACAAA TATGACTTT TGATATTATT AATATACAT
16651 GAAGATGTAA ACATTTGGAA GATCTGTGTA AACTCAACCA AAGTATGATG
16701 TTAGGAATTTC TGCTGGTAA AGAGATCCAT TGAAGAGCA AGATCACCAA
16751 TGGATTTTTTT TTTTCTTTT TTTTGAGAC AGTCTGTCT TGTACCCAG
16801 GCTGGAGTCAAGTGGCACAA TCTTGGCTCA CTGCAACCTC TGCCCTCCCG
16851 ATTCAAGCGA TTCTTCTGCC TCAGCCTCCC GAGTAGCTGG GATTACAGG
16901 GCGCTGCCAC ACTCCCAGCT AATTTTATA TTTTAGTAG AGACGGGGTT
16951 TCGCCATGTT GGCCAGGATA GTCTCAATCT CTTGACCTCA TGATCTGCC

FIGURE 3E

17001 GCCTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACTGCACCTG
17051 GCCTGACTTT TAAATACTAA ATGTATCAGG GACTTCCTGC
17101 CTCTTATGGT GTGGTGTGAC TTTATGCTG TTCACTTTGT ATCTTCTGT
17151 TACAGGGTTT GGGGCTCTG TTATATTAT TATTATTTT TAATTTCTC
17201 TGTTCTCTTA CCAGTGTGTT TCCGTCTTG TTTGGTTGT CATCTCTGT
17251 TGCACTTTTG GGATCTGAAT TTTTTTTT TTTGAGATG GAGTCTCCCT
17301 CTATGCCCTA GGCTGGAGTA CAGTGGCAGC ATCTTAACTC ACTGCAAAC
17351 GGAGCTCCCG GTTCAAGCA ATTCTCTAC CTTAACCTCC TAGAAAGCTG
17401 GGATTACAGG CACATGCCG TATGCCCTGC TAATTTCTGT ATTTTTAGTA
17451 GAGACGGGT TTCGCCCTG TGGCCAGGCT GGTCTCGAAC TCCCTGACCTC
17501 AGGTGATCCA CCGCTTCCGGC CTCCCAAAGT AGTGGGATTA TAGGCATGAG
17551 CCACTGTCGCG TGGCAGGTC TAGGCTTTA CAGTGGTCAG TTCAGTGGTT
17601 AGAACAGAC CCAAATACAC TTGGAAAGGA TAGAGTGTCT GAAGAGAGTT
17651 GGAGCACCCCC TCTGGTCAA TCTCTGAGAG AAGGGATTCT CAGAAATGTC
17701 AGAGAGTGGG GACTTACAGC ACAGTGGATA AGAGGGGGAG CTCTGGAGTC
17751 AGACTGCCA AATTGAATC CTGCCCGAGE CCTTTACTAG GTATGTGACC
17801 TTGAGCAAC TGCTTCTCATCA TCTATAAGAT AAAATCTTAC AGGGTTGTTG
17851 TGAAAATAAA ATAAGATAAT GCATATAAAC ACTGAGATCC TAATAAAAGT
17901 TAACTGTCAT GGTTATCATT TCTTGGCTG TCTTCCACTT CAGATGGTT
17951 CAGAGCTTGA TCCACCTGTT AAAAGGCAAC ATTGGCACAG GACTCCTGGG
18001 ACTCCCTCTG GCGGTGAAAAA ATGCAGGCAT CGTGGTAAGG GTCTGCATCA
18051 GTGGAGAGGA GTGGTGACAA ATTTTAGGG AGTAGCTTTT GTGTTGTTA
18101 AAATGACTT GCTTTAAACAT ATTTTAAATA GAGAACATT TTAAAAAAAT
18151 CAGTGGACAA AAAGCGGAAT TCAGACATTTC ATTCACTTAA AGATATTAT
18201 TTGAGAGTGT CTGTTGGTTA GGCAGTGTGTT TAAGCTCTT GAATACATCA
18251 GTGAAATAAA TATTCTGCCG CTATGGAGC TTACTTCATG GTGGAGAGGA
18301 TGTAAGTGGAGA TGGCTCGAGC AGTTCTGTC AATAATATGA ACTAAATGAGT
18351 TAGTTACAGA TGCTTGCCCA TTCTTCTACAG TCTCCCATGC CCTGTTCTA
18401 AATGGCCAAC TGGCAAGAATC TTATGTCTTC TTCTTGAT TTACCTCCAG
18451 TTGACTGCTT GCCCAGAGCC ATTCTGGTTT TTTCGGAGT TGAAGAGAGA
18501 CTCAGAGATG TTGGGTTGCCA TTAGCTTAAGT GCAGTCTTTC TTGATCTGGC
18551 ATTGCTGTAA AGATAACTTA CCCGCTCTCAC CTACATCCC TTAGGCCAGC
18601 TCTCCCCACA GTCA CAGGAG CTTCTTATTC TGCTGATGTG CACCA GTCTT
18651 GGAACNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18701 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18751 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18801 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18851 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18901 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
18951 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19101 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19151 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19201 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19251 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19401 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19451 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19501 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19551 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19601 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19651 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19701 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19751 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNN
19801 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNTGTTCT GTGGTTAGG
19851 CACTGTTCTA AGCTTCTAGA ATACATCATG GAATTAATAA TTCTGCCCT
19901 CATGGAGCTT ATCTCATGGT GGAGAGGATG TACTGAGATG GCTCGAGGAG
19951 TTCTGTCAA TAATATGAAT TAATGAGTTA TTACAGTAT GTCTGCCAT
20001 TTCTACAGT CTCCATGCC CTGTTCTAA ATGGCAACT GCAAGATCT
20051 TATGCTCTT TTTGTGATT TACCTCCAGT TGACTGCCGT CCCAAGCCA
20101 TTCTGGTTTC TTTCGGAGTT GAAGAGAGAC TCAGAGATGT GGGTTGCCCT
20151 TAGCTAAGTG CAGTCTTCT TGATCTGGCA TTGCTGTAAA GATAACCTAC
20201 CCGTCTCAC CACATCCT TAGGCCAGCT TTCCCAAGC TCACAGGAGC
20251 CTCTTCTCTC AGCTGACTAA ATCTCTGAA AATGTGCTAA AGTTCAAGATA
20301 ACACCCATCT CACAGAGCTA ATCTCCATGA TCACGTTCT CTCTCTAATG

FIGURE 3F

20401 CTGGGCCAA AGTTTGTCAGTAACTG CTTAGTAGC TTTTAATCC
20451 TTGTGAACT GAGTATCCATTGGGTTCTCCTAATTC CCACTTTTC
20501 TCTCTCTT GGCTCGAA TATCTGCCCCAGATGGGTC CCATCACCT
20551 GCTGATCATAGCAGTCAACCGGGTACGTCATGGTAAAT
20601 GTGCTCACCAGCTGCGCAGGTGAGAGCCTCTGAGCC ACCTCTCAAG
20651 TGACAGATTGCTTTGGGTTCTGTATACACCTGAAACCTGAAAATGAGCACTG
20701 ATGCAGACCACTCTCAATTCTTACACTGGCTGGAGGTAGCAGCTTATGA
20751 TTGAGCGTTTTCCTTGGGTTTGGGTTTGGCTCAT
20801 TATCATCTGTAAATTTACTTATGCCAGGGTACTACAATTC
20851 ATGGCGTTGTAATTTACCCCATTGAAAATGTTACCCAGATGGTTG
20901 TAATTATAATAAAAGTAACCTCTGCTGAACTACTTCTGATCTTTG
20951 AAAGCACAGATACAGGACTCAGAGTGTGACCTCAGGGTGAAGAGTGG
21001 AACTGGCCCAAGTCTAGTGCTCTTTTGTTCTGATTGCTTGTCT
21051 AATCCACGTTCTGCTCTGCTCTTCTCTCCTACTCTCAGGGCTGAAT
21101 AAATCTTGGTGGATTGTTGATAGTGTGACAGAATCCAG
21151 CCCCTGCTCCGGCTCCGGAAACCACGACACTGGGGAAAGGTAACGTGATT
21201 CCTCTCTCTCTCAACTGTGCTGAACTACTTCTGATCTTTG
21251 GGTGCAACGTTGGAGACAGTGTAAAGCTGGAAGAGTGCAGTGGG
21301 AGTTGCTTGGCTGGCTCTGCTGAGCTCTGCTGGTAGTAAGCTGTGACCT
21351 GGGGCTGGGTAACCCCTTTTTCCTGGGTTTGGAGTTTCTTACAGGAA
21401 AGCATGGGGCTGGCTGGCTGGCTAGAGCCATTGCTTGGGG
21451 TCTATGACCACTGTTGATGTTTGTGATTCACTTCTTCAACATGTAT
21501 TTAAGCACTATCTTAAATGGAAACAAACAGTGTAGGTAAGAAGGGAA
21551 GATTCTCTGAGTAAATTATGTGGTTCTCACTCTCAGAGGCTGTAGTC
21601 TTGTTAAAGGAAAGAAAATGTTGGAAAGAGAAGCCGGGGAAAGATAAAGA
21651 GACCCAGTGTGGGAGACACCATAAGAACAGAAGTGTGATCAGTAGGAGT
21701 ACACCCCTAGCTCTGAGAGAGGACTTAAAGATTCTCTGCTCGC
21751 TTGTCAGAGAGAAACGCACTGAGAGATAGGAGCAAAGAAGGCTCAG
21801 GAGAAAGGTGAGATAAACTAGAGCAGGGCTGGAGATGAGTTGGAGGTGG
21851 GAAAGTATTGCAAAATTCTCTGTTATGTTAACTCTTCACTGTTGGAGGG
21901 AATATTATGTTGTTTCTACATTAAATGTTGAAATTGATACATCAAA
21951 GGGCTAAAAAAATCTTAAAGAAAAGAACACATTAAAATGTTGATC
22001 TCTCTGAAAGATTTCTTGTGCTCATAGGAAACTTCTTCTTCAAT
22051 ATAGTCACCTTATCTCTGATGAGATTAATGTTCTTGTGCAAT
22101 TATTTCTGTAACTGGGGAGAGCTAGATTGCGAGTGTGACCATGAGTT
22151 GGGTGGGTTGTAATTCTCTTCTCTTCTTCACTACTCTCTTCTC
22201 CGCCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
22251 TTTAAATGGCTGCTCATAGATAAAACTTTGTGATCAAGATTAGGACATA
22301 AAGTAAAAAGTGAAAGAAAAATTTGGTCACAGTGCATGGTAGCTTT
22351 GGAATTTGCTGTATAAGTAGAACACATACACATGTTCTTAAAGTTTTTG
22401 ACAGATTGACCATACATGTTGAGCTAGTTGCAAGGTGACCATGAGTT
22451 AACAGTTCGACGCTTTCCTATCAGGAGTAAACACATTCTC
22501 TTTAAACTGCTGTGATATGTTTAAAGCAGTCTAATTAACATC
22551 ACTCTGCTTGTGATGTCCTTGTAGGTTGTTGAGCTGCTATTGTCAC
22601 CAGCAGTCGTTTTGGTACATCAGTTCTGTGCTTAAAGGGCTT
22651 GGTTGGTCTTATATCAGAGTTATAGAGACAGTGAAGGGGACTATTCT
22701 TTGTTTTATGTCAGGGTAACTGGTAACTGAAACAAAGATGGAGATGG
22751 GATAGGTGGGAGATGTGTAAGGAGGATGCTAAGGGGCTGGCAGTGGTC
22801 ATGGTGTCTGTGATGTCACACCTCATGAGCATTCCAAGGAGAAGC
22851 CAGGAAGGGACGCTGGAAACACAGATGACACTCTCCATTCTT
22901 CCCATGCCAGACAGTCGACACCTAGCACTGGCTTCTTCAGG
22951 GCATCTCGTCCTGTCACTGCGAGGAGGGTCTGTGATGGCTGGGGAA
23001 AGCAGTGTAAACAAACACTTAATGGGACACACTACACTGTTGGGTGA
23051 TGGGTACACTAAACGCCAGCACTACCATGAGTACATTGAGTAT
23101 CAAAACAGCACTTGACTCTCTAAATCTTAAACAAACAAACAAAAAA
23151 CACCTCCCTCTGGGAGCTGCTGATTGTTGAAACAGTCTTGTATT
23201 CCTTCTCTCCACCTCCAGACGTTGTTGACTCTTCTCTGATGTCAC
23251 CGAGCTGGGATCTGCTGTGTTATTTGTGTTCTGGCTGACAACTTTA
23301 AACAGTGTAGGACCTGGTAAAGAGAAAAGAAAACAAACAGAGCG
23351 AGAATGGCAAAGATGATTGAGTTGTTGTTGTTAGGATTCTTCAAAATCA
23401 GCTTTGTCAACAAAGAGTAAAGTTTCATTTTACATAGTCTAGC
23451 TCTTCTTATTGATTCCCAGTAAAGAGCTGGGCTAGAGAAACGCCAC
23501 ATGCTCTGTCGACCCCTCTGCTCTGAGTACCAAACCTAGCTCA
23551 GACAATTGGGTTGCTGATGAGTCAGTGTGAAATGTTCTAAAGTGGCTAC
23601 TGGCCACAGATCTTAAAGGCTCTGTTACACACCTGAGGCTTCTCAG
23651 GAACTCTTCAGCAGAGGATCCACGGCTGGCTGTTGAGGGTGT
23701 TCCGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
23751 CCACCAATAACTGCCACAAACATGAGAGCGTGATTCTGACGCCTACCATG

FIGURE 3G

23801 GACTCGCGAC TCTACATGCT CTCCCTCCTG CCCTTCCTGG TGCTGCTGGT
23851 TTTCATCAGG AACCTCCGAG CCCCCTCCAT CTTCCTCCTG TTGGCCAACA
23901 TCACCATGCT GGTCACTTG GTCATGATCT ACCAGTTCAT TGTCAGGTA
23951 CATGCCCTAGG CCCCCTCTA TCATCTTGGT TCAATATTIT AAAAAGCCA
24001 GGCGTGGTAG CTACGCCCTG TAATCCCCAGC ACCTTGGGAG GTGGGGGCAG
24051 GTGGATCACCC TGAGGTCAAG AGTTTGAGAC CAGCCTGGCC GTCATGGTG
24101 AACCTGTCTC TACTACTAAA AATAGAAAAAA TTAGGCATGG GGGTGTGGC
24151 CTAATCTCAAG CTATTTGGGA GGCTGAGGCA GGAGAATCGG TTGAACCTGG
24201 GAGGGGAAGG TTGCACTGAG CTGAGATCAT GCTACTGCAC TCCAACCTGG
24251 GCAACAGAGC AAGACTCTGT CTCAAAAAAA AAAAAAAA AAAAAAAA
24301 TATATATATA TATATATATA TATATATATA TATATAAAAT ATATATTTAC
24351 ATATATGTGT ATATGTTATT ATTATTTACA TATATATTAC ATGTATATT
24401 TACATATACA TGTAATATAT ATTATGTACA TGCTATAAT ATATATATA
24451 ATGTATGAA TATTATATATA TTATGTATAT ATATACATAA TATATATATG
24501 TAAGTGGAAAT GTAAATAGTT ATATGTTACT ACTGGTATGT CTAGATTAG
24551 GTGGCCCTG TTGACATTTT GGGATGGATA AATTCTTTC
24601 TATGGGGCTG TTCTGTGCT TGTTGGGGTT TTAGCAGCAT CTCTGGTCTC
24651 TCTCATTAGG CACCTCTTCA TGAGTTATGA CAACCAAAA
24701 TGTCCTCAGA CATTGCCAA CCTTCCTGG GGGCAAAATC GCCCCCCCAC
24751 CCAAGGGGGC CTGGTCAA CTTTTTCAA TTAGATGGTT AATTCTGAT
24801 CATTGTATAC AGTTGGAAA TAGAGAAAAA TGTTAAAGATT AAATAAAA
24851 ATAATTTTC TAACTCTGTAT TTAGATAAGT AATTCTTAT CAACTCCAGT
24901 TAATTTTTAT TTGTCAAAAT TATAAAATCA CTTGTTCTT GCCCTCACTT
24951 AACCCATGCA GGCAAGTCTG TGGGGTGGCA TGAGAGAGAA CATCTGTATA
25001 CAGATGGGTAA GAAAATCAGG CTGAGAAAAA TGTCCTTAA AACACTATGG
25051 CTGTTTGTAA AAATGAGAA GCATTTCTA AGGCTTGAGA AAAGAAAAAA
25101 AGTAAAAGCG GGTTAAATAA AGCATAACTT AAAAAGAAAAA ATACTTAAAT
25151 TCACTTCCC AAATAATTCA TCAGTACATA TTCACTTAA TGAGACAAAC
25201 ACAAAACTCTT CTGAATACC ATGTCCTTCA CCCGAGTCTC CTCTCAGGG
25251 CCCGCTGTAT TGATGGTC TGTCCTCATC TAGATCTGT GAATGGATT
25301 ACAGCCATG TAAGTATATT GAGAAATACA TTGAAATATA TTTTGTTTTC
25351 ATTTTTGAA CATAATTTT TAAAGTTACA TGTTCATCTA CCTTGTTTT
25401 TTCCACCTTA AAAATGCTT AGTGAGCCTT CCAGGTAGT ATTCTGGCT
25451 CTACCTTGT GTGTTAGTT GTCACATTGT ATCACAGCAA GGAGATTTC
25501 TGCCATTAT TAAACAAGTC CTCACTCAGT GGCTATCAGG CCATGGATAA
25551 TTTTGTAGT TATTCTAGTA TTAAAGACAGT GAGATGTTCT TATACATTCC
25601 TTTTGIGGA CTTGTATAAA TACTTAAGAT ATTTGTCTAG ATGTTAATT
25651 GCTGAAGAGT GTGCACTTT GAATTTTTGT TATGTTACCA AGTTTTTT
25701 TCCAAAGCTT ATTTCTTAAT TTCACTAGAGA CTCCCTTCA CAGTATTAA
25751 GTGCCATT TTCCATCTT ACTAATACTG GATGTATTAG TATTATTTAT
25801 ATTGTATTG TTGATATATG TATGATATATG TAGTATTAT ATATAGTATA
25851 ATTATTTAG TATTATTTG GTCACTCTGA CAGGTGAATA TTATCTCATT
25901 TTCAACAGT CTGCTTAAAC TGACCCAGT CACCCACTGA TATAGTTCC
25951 AGGAAGACAG TGCTCATATA AAAGCAGGAG TTCTTGCT AAGCAATGA
26001 CATTATCAAT TTAGATTAAC ATTTGCTCT GTGAGTATTG ACTGTTTTT
26051 CATCACATTA AGTCAGATGA GTGGCAGATA TTGACTCTTC TGCAAGACTA
26101 TTTTTTAAAC CATAAAATAA ATAGTTCTTC ACCTTCCCTT TTATGAGAC
26151 TGGAAAGGAGG GCGCTGTGAAT GCACTATAGA CCATTCTCAT TACCAACAA
26201 GGAAGGGTAA ATATTTACCC ATGATTCTCAT GTGTAATTGA GAACTCTAA
26251 GAGCACCTAG GATATACTCT ACCTGACACT AAAGATGAAT TGAGTGGGC
26301 CACCCCCATA GACAGACACA CCTGCTGCT TTACTTTAA ATCATTGAG
26351 GTAGTCGGC TGTTGGTTT GCCATGATCA GAGGGCTGGG ATAAGAATT
26401 GGGTTCTTAT AGCGCTCTAG TCCCAACCAA CTGGTAGTAT CCATCCAGAG
26451 TGATGTCTAT GCATAGTACA ACCAGGACAC AGAGCAATGT CTGCATAAGG
26501 GCAGCCCTGC TGATTTCTT AGGACCAATT TGAGTCTTCC TCTGGGCTTA
26551 GCGAGAAGT GTGCTGTGAT CAAATAGTC CGTCTGCCT GAGTACAGCA
26601 TGGGGGAAGA GTTTGGCTG TGTGTTGATG TAGTCACTGC CCATAGTGT
26651 GTAGTTGCTT CATTGTTGATG TGTCATACAG CTAAAGATGC TCCCTTTAGG
26701 TGTTGCTTGT TGCCGCTGCC TCTGGGGTT GTTACTACTG TTCTGTTTTG
26751 GCATTTGCCC CCACTTACCA TGAGGATTC CCTACTGTC AATGTTTCTG
26801 AATTTTTCTC CTAAATCTAA GCATGTACAT GACTGTTCC CTTGCCCTC
26851 ATGCACTGCT CATTGTAAGT AGCAGACCAA GTCTTCCAC AGAGAGCAGG
26901 TTCCCTCTG TCTTCAGCAT GTGGAGTCTC AAATGGAACA GTTCTGGCA
26951 GAGTGCTTTG CACAGAGGTT GCTCCCAATAA AATGTTTTAT CACTGCATAT
27001 CGTTGCTTCT GAGATGTTATT TTGTCATAGT TATAACAGTT TCAGGATTGC
27051 AAGAGTACAT CTCACAAATCC ATGTTGACCT TTAAACAGCAT TTTCTCAAAA
27101 TACTGTTATT ATAATTGATA ATATGTAAG ACCTCACTTA ATATCATTGA
27151 TACATCTTAA GAAACTGCAA TACATTAAT GTATGTATAG CGAAATCAGT

FIGURE 3H

27201 TTTTTCTCA TCAATGTTAT AACAAAACAG CGTTGAAGGA AGTGAAGTGA
27251 CGTCATTCA CTTAAAGTCT CAGTTCCAA GAACTTATTG ACGACAAGGG
27301 AGGACTTAATC GTGTTGAGA ATTGAGGAGA TATGTTAATA ACGAGCTGAT
27351 TTAAACATGT ATGTTCTTT ATAATTAAA CTTTCTCAT TTAGTTGGTT
27401 GGGTCAGTAG CAATCAGTAA GTATGTTAGA TAATACACTT CTTCTGCTGG
27451 CCTCATTCCTT AACATATCCC CACATATGGA TTGTTGAAATT CCCAGTCTGA
27501 TACTTGAATC TGATCTGATG TATGAAATAAG AGCAGGAGTC ATTCACTAAC
27551 CAACAGATAG CACCTGTTT CAATAACCTA GTTACATTGTT GTGACTCAGG
27601 ATAATTACCA GGCCACTT GCTCTCAAGT CCCATTGTAAG AGGAAAAATA
27651 CCTTATACCC TGTCCTT CCAAGGTATTG AAATGCTTCT TACAAAGGGA
27701 TCTAACAGAT TTCTTAGCAG GGGCCCAAGGG AAAACACATTT ATTAAATTIT
27751 TTATTTTTT CAAAGCAAT ATTACTGCTT TGAATCTTT CAAAGTGAAG
27801 GCTGTTTATAG AGCTTAAATG TGATCTCTT TTACTTGCC TTGAAATTATT
27851 CTGAAGCTG TAAAGAGCAT GCCCCGTAT ATCCAATAG CCATACAGTT
27901 AAATCAATTG TAAACACATTG TAAAGGCTG TTTAAACATC AATTTTATT
27951 TTAATTGAG CAACATACAC ATGTGTTTA GAAAACCAAAT TTGTTAAAAG
28001 ACAGCAGCTT TGAACTCCCT CTCCCCACCC TGCCCCCTCC ACACAGTCTG
28051 TTACTGGAGA CTGTTGTTG TGGAAGGATT TTGTTGACTAT ACCTCTGCT
28101 TAGCTAGGGT TCTCTAGAGG GACAGAACTA ATAGGATAGA TGACATATA
28151 TAGGGAGGT TATTAAGGAA TATTAACCTA CGCAATCACA GGTTTCCACA
28201 ACAGGCCGTC TGCAAGCTGA GGAGCAAGGA AGCCAGTCCA AGTCCCAAAG
28251 CTGAAAGACT CGAGGCTCTGA TGTTCAAGGG CAGGAAGTAT CCAGCACGGG
28301 AGAAAAGATG AGCCCTGGAG GCTAACGGCA TCTAGCCTTT TCACATTCTT
28351 CTGCTGCTT TTTAATCTGG CCACTGGCCG AGCTGGCAGC TGATTAGATT
28401 GTGCCATCC AGATTAAGGG TGGGCTGTCG TTTCCCAGTC CACTGACTCA
28451 AAATGGCAAC CACCCCTCACAA AACACAGCGA GGAACAAATAC TTGCCCCTCT
28501 TCAAGTGAAT CAAGTGTACA CTCAGTATTAA ACCATCACAA CCTCCCTCT
28551 TATACAACCT TAACATTGTA CTCAGCTGTTA ACAGTTGCCCTT TTGTTCTGGC
28601 CCATTTTTA AAGCATTCTT TTTGCTCCTC CTCCCCACAT GTTCCAGCAC
28651 TCCCTGTTG TGCTTCTTGG TAATACTTTG AAAGTGTCA AGTTCATTTGA
28701 TGAGAATTTC AAAAGGAGA AGAAAAGAGA AGGAAAAGG AAGAGAACCA
28751 ATATAAAATG GTACCACTT CTCCTCTT CCAAGCTTAT CTTTGATGTT
28801 TATGTTAGTG TATCAGAGT AATATATAAA TTAAAATTAA AATTTTTCT
28851 CACTAATATT TCGTAAGTAG TTTTCATGT TCTACTTAAAGT TATCTCAATT
28901 TTATGTCAT AATAGTGCAT ACTGGCAGG CGCAGTGGCC AACGCTGTG
28951 ATCCCAAGCAC TTGGGGAGGC AGATCAGTCA GCTCTGCTCT ACCAAAATA
29001 TTCAAAACA GCTTGGCCAA CATGCTGAG CCGCTGCTCT ACCAAAATA
29051 TACAAAAAAATG AGCCAGTGT GGTGGCACCG ACCCTGATGC CTAGCACTC
29101 AGGAGGCTGA GGCAAGAAGA ATTGCTGAA CCCAGGAGGC AGAGGGAGGT
29151 TGCACTGAGC CGAGATCTCG CCACTGCAACC CCAGCCTGG TGACAGAAGG
29201 AGACTCTGC TCTAGATAGA TAGATAGATA GATAGATAGA TAGATAGATA
29251 GATAGATAGA ATATATATTG TGTTGTTAG CTGGTATGTT GTTAATTACT
29301 TAACTGATCTT CTGGTTGGAG AGCACTTAA TTGTTTGGAG TTACTTTATT
29351 AAACAGCTT GCTCACTGTT TTTCATCTT TGATTTTTT TCTACTTGAA
29401 TTCACTTCTT GGGGATGGGA TTACCTAGTG AAAGAATGTG ACTCTTTTA
29451 TGCAAGCCCTT AACATTGGAG TTTTTAAATAG TACCTGGGGC TTGTCCTTCC
29501 CCCAAACAAAG TGGGTTTTC TTAGGCTGAA GAGAAAAAAAC TACAAAGTT
29551 AAATGTCCTT AAATCATCTG TCAGGTATTAA GACTTTCTC CTTTAGAGAA
29601 TCTTGGATTG TTAAAGAGT ATGACCTCTC CGATTCAAGG TTCAAATCTT
29651 GAATTCTGT ATAGCTTTT GCTTTGTTT GCTTTCTGTC TTTCAGAGGA
29701 TCCCAGACCC CAGCACCTC CCCTTGGTG CCCCTGGAA GACCTACCT
29751 CTCTCTTCTT GCACAGCGAT TTTTCATTT GAAGGCATTG GAATGGTAAG
29801 AGCTGCACTG TGATTTGGC TAGTTGTTCTC TTGGTCCCTT GTGTTCTCC
29851 AGGTCTGTTT CAAGGAATGC TGAGGAAACA TTGTTAGAAA GTATCTCTG
29901 AGGCCAGGCA TGTTGGCTCA CGCGCTGAACTT CTCAAGCACTT TGGGAGGCC
29951 AGACTGGTG ATCACTTGG TGCAAGGAGT CGAAACCCAGC CTGGCAACCA
30001 TGGTGAACAC CCATCTCTAC TAAATATACA AAAATCACTG AGGCATGGT
30051 GCACACGCCTT ATAATCCCA CGCACTCGAGA GGCTGAGGGCA GGAGAATTGC
30101 TTGAACTGGG GAGACGGAGG TTGCAAGTGC CCAAGATCAC GCCACTGCAC
30151 TCCAGCTGG GTGACAGAGC GAGACTCTG CTCAACTGGC AGTTAGTGAAG TGTGTTCTG
30201 AAAGAAATTAA TCTCTGTAA CTCACTGGC AGTGTGAA TAGTGTGTT
30251 GGGATTCTCAT TGAGATTTCC CAGCTTCAAC TTTTCAAGAC AAATTATATG
30301 TAATTTAAATG TGTTTACAT TCAAGGCCCTT CTCACTGCAC ACTCATCTCC
30351 TATGTTGTGCA TGAAAGGAATA GCATATGGCA ATCAGGAAGG CAGGGCTAG
30401 AGTCAGACTG ACATGGGGGT AAGTCCTGGC TCTGCGATAG AGTAGCTGTG
30451 TGACCTTGAG CAAGGGCTTC ATCTCTTGA GCCTTCATTA TTGTTCTG
30501 AAAATGTGAGC TTAAATGATTC TGAGTTTAAAGG GATTAATAG AGATATGTG
30551 AAAATGCTTTT GCACAGACCC TGACACATG TAAATGTTA ATAGATTTT

FIGURE 31

30601 ATTTTATTAA TAATGTTATT TTATTATTGA ATCAATAAAT GCATGAATAA
30651 TTTCTCTGCC CTACAAACATT GGTTGGGTG AATTTCTCGC TGCAAAGAG
30701 CAGCCTTCAC TCTGGCTCA GCATTTCTGTG ATTTCAACAA ATGTTTCC
30751 TAAAAAGGA TCTACCCCTC ACTTTAACCT AATTGAATT TTATTTGTAT
30801 TTTTCATAAT AATGGTACAA AACCTTCTTC TGAAGAAAAGT TATTCTGGC
30851 CAAGGGCGCC ACAAAATGGG AGAGCCTCTT CCCGGCACGG CACTTCTTC
30901 TCTTTTTGA TTTCGAGAC ACCTTATTTG CTTTAAGAA AACCTAGAAAG
30951 CTGTACACAT TTTTGCAAA AATCGTGAGA AATCACCCAG GTGGTGTG
31001 TGAAACACGT TGAAGCTGTG ACATCATGGG GGAGGCTTTG GGAGTGATCA
31051 CATGTAATC ACTGGTCTCC CTGAGGTTT ATACCTTGCC CTGTGCTCTA
31101 TCTTAGGGCT TTTCATTGCC CATGAAAGGT GTCTCACTGT AATTCAAGAAA
31151 CACAAATGGT TTCTCTGC TGGGGCACAG GCTGTGTTTGG GCCCATCTT
31201 CAGCAGTGC AAAAGATCC AAAGAACTCA GGACTGAAAGA GAAGGGCTG
31251 AGAAAGTGTG GAAAGATGCC CAGAGACCTT AGGTTCTTG GCATCTAAG
31301 GGACCTTGTG CTAATTTT AGTAGCTTTC CCTAACAGCA CAGCGCAGAA
31351 ATTGTTGCT GTGGTTTATT ACCCAAGACT TGACACAAA GTTATTTCTGC
31401 AAACATCATT TGTTTCAAG ATTCTTTGT ATTCTTATT TTTCACAATA
31451 GAGAGAAC ACTGCTAGAT TGACTCTTAG TTTTGATCT AGGGCTGTT
31501 CATTGATCG GGGTAAAGTG CCAGGCTGCA CACTGTATTC ACCGTGTGCT
31551 CTGTGTCAT GCAGCTGCA CAGGCGAGAT ATGGCTCCC TGCCCTG
31601 CTCTTTGAT TCTGGTATG ATGGAAACTG ACAGATACT TTAGAAGCTG
31651 TTCTAATGG ATGGGATTA ACTGAAGCTG GAGCAGGTGG TGGGGGACAC
31701 TGGGGGCCCGC TGGGAGCACC AGGCCTGCAAG CAGGATCATG TTGGTGTG
31751 CAGCACAGAC CTATTTGTC TCTATGGTGC AGGTGTCGA GAAAATAAG
31801 TGTAAATAACAG ATGATCAAAGT TTGGGCCACA GTAGACATT GCCCCAGTGT
31851 GCTCTCTCTT ATTAGCTGTG CCAGATCCAG TTGATGGCAG ACTGTGAAGA
31901 TCCTCACAGT CACACCTGCC ATTTCACCAAA TTCTAAATA AACTCATTT
31951 CATAGGGGCC TTTCCTTGC TTTCACCAAA GTTAAAGAAT GTCCCTCTT
32001 ATGATGAAG AGGTAGCAAAG GGTCACTGG TTGTAATAGG AGTCTGGAAA
32051 CTGGCATTTG TTAAAGCACC ATGTCCTGAG ATCCCTACG AAGTCATGCT
32101 TTCTTCGCA CTGCACTGG TCTCACTGG AGGTTAACT TGTCACTGCT
32151 AGTGTGTCCTC CCGTGTGAGC TAGATGGCA GTTTCTCTG ACCTATATT
32201 TGCACTCTT AGACAGGTTA GCAGGAAGCT GTATCTCAG GTAGATGCC
32251 AGGTGGGCAT GACATGAGAG GGCCTCTGG TTGCCCATGTG GCCTCACTCA
32301 CAGGGCAAGC GACATTCCC GCCTGAGGG ATCTGCAAGC AGGAGGACAG
32351 AGCAGCTGCC TGAGCCAGGA GTCTGGCTGT CGTGTCTGT CCACCCCTTAC
32401 TTTAGGACT TCTCTAGCTG CCAGTGGGG AGGAGTCCC TTCTAGTCCC
32451 AAAGACATAAC CGTCTGATGA AATAACTTT TTAAAGAGC AGATGTGCTT
32501 CTGGAGAATT CTGGGGATAA AAGAGTTACT TTTTTCTGA GGTTTTTTTT
32551 TTCTTGCCCTT ATTAACTTTT CTCTTTCTG CACTTTCTC CCTCTCTCAC
32601 TACTCTCTCA TAGGTTCTGC CCTTGAAAAG CAAAATGAAG GATCTCGGA
32651 ATGTCCTCACT CATCTCTAC TCTGGCATGG TCATCTCAC CATCTCTAC
32701 ATCAGGCTGG GGTGTCCTGG GTACCTGCAAG TTGGAGCTA ATATCCAAGG
32751 CAGCATAAAC CTCACCTGC CCAACTCTG GTACGTGGAG GGAGGATGGA
32801 AACCTAGGAG CACTGGATAT TTTAAACAC TAATGGTCA CAGTGTGGAT
32851 TCTCCCTCTT ACTTATCTC TAAACAGCC CACTTCACTC TAGCCCCACCA
32901 TCCCTGCGCA CTGGCAGCCC TCACTGGCTG CCCTGGACTG CATTCTGTT
32951 GGGGAATTCA TGATGAGCCT TCTGCTGAAG CCATTGGTGC TGATCAGCCG
33001 ATGGGAAGC CATTCTCTC TTGAAAGTCA AGGCTCAGAA GGACGGAGTA
33051 TCTAGTCCAT TCTAGTAAAC CCATTCACCAAA TAGACAGGGG GATGGGAGGG
33101 CAAACCTGCA TTGATTTCC AGCATCGGT GTGCCCTCTCC CTGGTAGTA
33151 ACAGGCTTGA TATGCGATG GGACATCTC ACTGTGAGGCC GGGGATTGTT
33201 GGGAGTCCTT TTGTAACCTC CTGGCATTTG TGAATGTATT ATAGGGAAAT
33251 AGTGAGGCAT TTGAAATGC TTCTGAAAG GTGTAATGTC CCAGGGCATG
33301 TGCAAGAGCA CCATCTCTT TTGAAAGATGA ATCATCTCAT GGTGGAGAGC
33351 AGCTGGTAGC AGACACTGAG AAGCTTGTG AGTGTCTGC GGATCAGAAAT
33401 CAGCTTCAG TCTAGGCTGG CTGATCTGC TGTTGGTGTCT TTTTATTTG
33451 TTTGTATTG TTTTATTTA TTGATTAAAT TAAGACAAAC GCACTCAGTA
33501 TTTCAGGGG CTTTCCCGTT CAAGTACGAA CCAGGCTTGA CCCTGCTTAG
33551 CTTCCAAGAT CAGGTGAAT TGAGCACATT CAGAATGGTA TGGCTATAGA
33601 CCTGGATTGG CTTTTTATT TTTTATATT TTTTCACTT GATTTTCACT
33651 CGTGGAGCAT ACCAAATTATA TATATGGATG CAGTATGTG GACATTTGG
33701 TACATATGTA CAATGTTAA TTATCAAATC AGGGTAATTG GCATATCCAT
33751 CTTGTGCTA CTTTTAAATT TCCAAATGTT TCTGCCCTC CAAGAAGGAA
33801 GAGGCAAGGT GTAGCTGGT GTAACTGTG CACCTTCCCC TGGAAAGATAA
33851 ATGGATCGGG AGCAACAGAA GCAGGCCACA TGATCCGAAG CCATAGGAGA
33901 GAATCTGCT TCTTTCTAA CACCCCAAC CCAGCTGCTG TAACTCTCT
33951 GCCTCCATTG GGGTATAATT TATTGGCT TCCCTGAGG TGTCACTCT

FIGURE 3J

34001 CTAAGTCCAG ACTTCACAGC TCTCCAGAGG CTTGGGGCT GCTTTGAGTT
34051 TAATGATAGA GCCACCGAT GATTTTCCC AAGAGTTTT ATTATCTATT
34101 CATGGAGCAA GTATGACCT TTACAGACT CAGTCCTTC AACGGTTGTC
34151 TCCTGCTTAT AGCATAAGAA CATCTCTAG ATTTAAATT CAACCACAGA
34201 GAAACTCAAG GCACATATAC ACAGTCTGTA TTAGCACATT TAAATAGATT
34251 TCCGACAAGG GAGGACAAT TTTCTTGCT GTTAAACACA TGAGGGCTG
34301 GTTAAAGGTG GAGCTTGCT TAGGGACAGA GACCTTTCT TTTAATGACC
34351 AGGTCAAGATC TGAACTGTA TCACAGACTC TTTCTACT CTGTCAGTC
34401 AAGGCACTGG AGTAATAAAA TAGGGATATC CTGTCAGTC TTACGTCTT
34451 TTGGAAGCT ACACCTGAAG CAGTAGTAGG AAGAGGCCA TAGGGTATG
34501 GAAAGATGGG ATTCCTGCTC GGCTCTGG TCCCTGAGT TCTTCATCTA
34551 ATTCTAGGG AACTGACTTG GATGGACAG ATATAAATAG GCTTGTGACA
34601 TTTAATTGCA AATTGGTT TTATTTGTA AGGCATGTAC ACCTGTATGC
34651 CCATGCCAAAG GATTGAGATT TCCAAGAGT ATATAGAGAG CTTAACGTT
34701 CCACCCGGCG CCCTCCACTC TAGTTCCAA TTTTCAATT TCCCATTC
34751 GAGGCAACCA TATTCCCAGT TTCTTTTGT TTGTTTGTG TGTTTGAGA
34801 TGTTTAAGTGT ATGATTGTC TGTTGGGGTA GTGTTGTTT TTCTCTCCTC
34851 TTTTTCTT TTTAAAGACAA ATTGTAGCAC TCTGTAGGTA CTGATTGCT
34901 TCATGCTT TTCACTTAA AAAAGTATAA TAAACTGTC CCCATGATAG
34951 TGATATGCTA TATCATGTA TAGAGTATA TATCATGGGG ATAGTTTCTAT
35001 ATCACACCAT CACACCTAGA GTTCTGCTTC ATACTTTGTT AAAAGCTATA
35051 CGGGGGCACC ACGATTTAC TATCGAGTTC CCACTGGTT ACATTTAAAT
35101 TGTTTCAAGT CTTTCTCTT TAAATATG TGCACTGAGA TATTTGAAT
35151 ATAAGCTTT GTGTATGTT GTAGGAGATA CTGTTGAGGTA AATTCTAGA
35201 CATGAAATTG CTGGTCCGA AGGACATGTG GTTTGTATC CTTGATAAGT
35251 GTCAAAACAT CGCAATGGGA CCATTGGCA CTCTTGTGCA TGATGTATAA
35301 GTGTCGCTGAG CAGGCTTGGG ATGTCCTCG TCTGTTGGG CAGGTTGTC
35351 CAGTCAGTTA AGCTGCTGA CTCCATCGGG ATCTTTTCA CCTACGGCACT
35401 CCAGTCTTCAT GTCCCGCTG AGATCATAT CCCCCTCTTT GTGTCGGAG
35451 CGCCGGAGCA CTGTAGGTTA GTGGTGGACC TGTTGTGCG CACAGTGTG
35501 GTCTGCTGA CATGTAGTA GAAGATGATA ATTGCTTGC TTGTTTTTCC
35551 CTAAAGGGCA CCCAGTCTGC AGGCTTTCAT GAGAAAAGAC AATGTTGTT
35601 GTAGTGAAAGC TGGCTATGTT TGTGACAGAAC AACCTGGCCC ATGGCTTC
35651 TTTCAGAGTT GAGGCACCTC CAGATGGGG AGTGAATTAA TTACATATGT
35701 ACTGTTAAAGA ACATGGGAAT GAGGACAGTG GTTTATGAT AGATAGGGTA
35751 TGAAATGCTG TGGAGGTTGGT TATCATTCAAG AGTAAAGACA TGCGATTACT
35801 ATCCCCATATT AAATAAGGTA AAGGCTGAA AGCCATTAA CCCATATCTG
35851 TAATGAGTAT AAGTAACTCT GATGAAAGGT ACTTATTGTC TTTTCAAAAT
35901 AGTTGTTTT CCACTGTGAC AAGTTGCTC TTAGATTTC TTTAGAGGCT
35951 TTATGATAGT ATTCTAGACA TTTTTAAATG TCAGTCTTC TAAATATGTT
36001 TCAGAAAAAT TCTATTGATT AACCTAGTAGG TTGATTGAT CACTTGTGTT
36051 TTATCTCTT TCTCTAACC CCATTCCCAG GAGTGAATG TAAAAGACAG
36101 GATACCCCTC TGTGTTGCTG GTTGTGAAAC TGTTGACATT TAGAAAATAA
36151 AAGTAAATT TTTTGATGAG TCTGTGAGT TGGTAGACTA GAGAACCCCT
36201 GAGCAATCG GTTGATAATAA GCTAAATTAA GTTTCTAAGA GATTGCAAT
36251 TGTTTCCAA ATTCAAATGCA TAAAAGCAT AGATTCCTCT TTTTGGCTCT
36301 ATTTGGCTT TTTTCTCTT TTAGGTTT ATTATTTTG AACAAGAACCC
36351 TCTTGTCTTA TTATGTTGAG ACCTCCCTGA GAATTTCTT AAATTATTC
36401 GTCTGAGCCT CTGCTTCTGG GATAAAAGATA GATCCATATG ACTTTTTAAA
36451 TTCTAATTAG GTTGAATGTT TTAAGGATG AAAGATGGGA AAGTTGTCTA
36501 GCATTGCTC TTAGTCACTC CTTCAGGGCC TCTCTAGAC CAGCCTATAT
36551 AGAAACAGCC CACGCAGCGA CTAATCCAGG GGCCAGGGCT GTTGAAGGCC
36601 AGCTGCTGT CCCACAGCGA CTGAAAAGA AGGAACATGA TGATCTGC
36651 TTTCTAATAA GATTGCTTA ATGTTGCTG CTAAGATGGG ATCTGGAC
36701 TGAAATTCTT AATCCTATCT GTGCCAGTA ACTCTCCATG CTTTGATTC
36751 AAAGTGTATG TTCTCACCGT GGATGGAGTA GCTCTAAGT CTTGAGGAGA
36801 CAGCTTCACTC GTGTATGTTA TTATTAATGT AAACCTGAG GGCCCAATT
36851 TAAATCTAA AGGGCACTGG AAGAAAGAT GTGGTTAGTT CAAATAATT
36901 GCTTTTATCC AAAGTGTCTC CTCCGGAAA AGTAGGCTC TGAGGTAAA
36951 ATGTGCTTC CTGACTAAAC AGTCTCTCA CCTGCTCTAT TGAGCTGGGG
37001 CAGTGACAGG AGCCTGACTC CTCTCCCTGC CCAATTCTT CCTCCAGCCT
37051 GGCTCAGCCTC CCCTGTAGCA TATGTCACAC TTCTGCCCCAG GTTATTTCT
37101 GCAGCACCTC GCAGGAGACA GCAGTCTCT ATTCAACAGAC CTATGTTAT
37151 CCTTGTAGTC CTCTGGATT TTGCTTCACT TTCTCTGGCC CTGTCGTG
37201 GTCTCATCTC CCTTCAACAG GACGATGTCTC AGAAGACACG GCTGCTTTTG
37251 GTCTCAAGT GTGTCAGTT GTTCTTCTCT TCTGTGATCT GTTGTGACTT
37301 AGCATTGCACT TGTGATCTG TTCAAAAGG CAGCCCCCTT TATGTCGTG
37351 AGCACTGCC TCTCTCACCT TCCCTGGAGA CTTGAAAGTA ATTGTCGGAC

FIGURE 3K

37401 TCAGTAGAGG CCTTCATGG CAGCAGCAAC TAAATGTAT TTATGCGCT
37451 TCATTTGTT CTGCTTCTC TGTTCTTC GATCTTCAG CACCGTTGGT
37501 TAGTATGTGA TTTAGATCT TTAATTGATT TTTTCTATT ATATTCATAA
37551 ATTTAACAG CAGCTTCTT TATTACTATT TCTGGTGT TCCATCTTT
37601 TCCCCAACTT TTCTCTTCC TCTTCACCC CAAAGGGAA CAGGAGGAAT
37651 TCAGTGTAGT TTCTTCTTCT TTTTCTCT TGGAAATTCAA CTTTCTACC
37701 ACTCTCCCCC ATCTCTAAA GATTACTATG GCTGATACGG ACTTTGTGAT
37751 GCTTAATTC AACAGTGGG AGAAGAGGG GAGGGAAAAC AAGTATTC
37801 TAGGATAGT CTCATTTGT TATGATTCA TATCGGACAG TATCTACTTC
37851 CAGCCCCATAT TTTGGGAAAT GCGGACTTAG CAGGTACCT TATGTCAGA
37901 CCTTGTTGG AAGAGGCTGG CCCCACCTG GGAGTCTGG GTGTTAGGAT
37951 CAACGGTTT TTAGATTCT TTGGACCAAT AACCCATCCA CTTCTCAGT
38001 ATTCTACATG ATTCCTGTG TATTTGCCA TGTGAAACAT TTAACTTCAG
38051 TTGCTATGA AAATTCAGA AACCTATTC TGAAGATATA ATTACCTAA
38101 ATTCGATCAT CCAAGAAGCC TGTGCACTG GGAATGCAGA GCTGCAAAC
38151 ATTCGAAGG TGTGGATTT TAGAGGATGA AGCTTCCAGG TCCAAACAGA
38201 GTAGCTCTT AGTACCTTG GGCCCTTCAC ACTTTTACTG TTGCGAGCTA
38251 CAGTGAAGAG GAGCAGCATC ATTAATTAGC TGTGTAACCC TGCCACCCC
38301 CACCTGCAT TCCCCGGCA GGAACCTCA TAAGGCCTCA GGGTCTCAA
38351 CTGTAAGATA GGAAGGGTGT CGACCTCTA AGGTTTCTC CAACTCCAA
38401 ATTCCTGTAG TCTGTATAGG TGCTTGCCTG TTGATTAA GTTCTACAC
38451 AAAATTACT CAAAAAAAG AAAGTCAATG TAAAACATT TGGGAATAAA
38501 AGAAGAAATT CGAGTATCC ACCAATTAA CAAAGTAATT TTTTTGCA
38551 TTGATCTTC TGTGTCTTAA TCCTCATGGG TGCCCTGAA AAATAGTTGC
38601 AATTGAGT TACACATAAT TTGCTTTC ACATTTTAT TAGTTTATA
38651 TCACAAATAT TCATATCTT CACTAATTT TTGATGACT CGTGGTATT
38701 CACTGTATTG TTGGATCATC TTAACTAAGG TACTCTTTC ATGTTGACA
38751 TGGTGGTGT TCCCCCTGTT TCGTATTAA TAAATTTAT ACCCCCACCA
38801 AGTCAAACTT TGATACTCTG CCAAGACTA TGTGAATT AAAGGCATAT
38851 TTATGACAT TAAAGTAA CATGGTAAA CCCCGTCT ACTAAAAATA
38901 CAAAACAAA ATTAGCCTGG TGTGGGGCA GTGCGCTGA GTCCCCAGCTA
38951 CTTGGAGGC TGAGGCAGG GAATGCGATC AACCCAGGAG GCAGAGCTG
39001 CAGTGAGCCA AGATCGCCG ACTGCACTC AGCCTAGGT ACAGGGCAG
39051 ACTCCATCTC AAAACCAATA AAAAATAAAA TAAAATAAAA TAAATAAAAG
39101 TAATCTGGTA AGTTTAAAC GCTTGTATCA TAATAATAA GCAGCAAGAG
39151 CTCCAGCAC AGGAGCCATA ATGGCCAGC GTATTCGTA AGTCGCTT
39201 TGTCTTTTG AGTGCTTGC CTTGTGTG TATAAGTCAG CTCTTCTG
39251 TGCTGGTTCA AAACCCACGG CTCCAGAATC CAGTCCCTT TGTAACATG
39301 ACTGTGGCC TTATGTTGCT CAGCAGTTT AAAAGCTCAT ATTCTTGTG
39351 TCTCTTGA CAGAAGGGAA ATGTTTGTG ATACTGTTG AGCCCTCTG
39401 ACTAATCATG TGTCGAGCT GAGGTGTG TCTGCCCC CTTTTGTACA
39451 CGCCACAGCT GAGCTGCTG TGAGAAGTGT ATAACGTCA TTGTTATACA
39501 AATGTCCTCC TTGTTGTCTG GGCTGGGTC TTGTTGTG TGGGGGGGT
39551 GATTGGGAG GAGTAGGGAG AGGGCTGTT CTGGCTGGT GCTTCTGAG
39601 ATATCTACCT TTGTTGAGT CTCTCATAG GCACTTAAAC TCACAGAAGA
39651 CATTCTGTC CAGAAGGGGG TTTATTCGCC CCACATGTCT GCATAGTC
39701 TTGCTGCTT TGGAGTTAG TAAAGTCATT TTCCATGGT GCAAAACAGA
39751 TACCCGTGCT GTGAACCTC GGGGGCTGT GATGCTGATT TGGTTGGAC
39801 ATCTCTCTC TCTTCCCACT TTGTTGTTAG GGGAGGCTCC CTCTCTTC
39851 CCTCTGCGT GTCACGGTCT ATGAGGGT CAGCGGGTGT ATGTTGTTCA
39901 GCTAGGACAG GAAGAAGGAC TTCCCTTGC AGCCCTGTT TCCCTGGCTT
39951 AAGGAGGAG AAATGTTCTT AAAATCTCA TTAAGGATAT TTTTATTAGG
40001 CATGTTTATC TTATATAGTG GTGAAACAA GAACAAGTTT TTAGATTACT
40051 TATAAAATAT CATGATGAAG CGGAAGATCT TTGTCCTC ACTTAACTCC
40101 TTCTGATCCC AACCTCTGT TTCTGTTCC ACTTAACTCC CACCACAGAG
40151 TGGAGCTCCTC CTCTGACTCC ACTTAACAT CATGAAGTGC CCATATGTCC
40201 TGCTAGGTC GATGGGAGA GGGTGGGAG ATGACAGACT CTCAGGGCTG
40251 GGAAAGGCTC TGATTTGCT CCGCCAGGG ACTCATTTTC TCTGATAATA
40301 AAGGCTCTC GTCTCTTGA CGGACATCAG CATTGTTGGA GATGCTTGT
40351 TGGCTGGGAC TGAGGAAATA ACTCACACTT CCTTTATCCA TACAAAACCG
40401 AGTGGGTTAG AAGCTCCCTT TTGGCAAGC CATGTGTTCG AGGCTTGGAG
40451 CCCCATCGCT TTGCTGTGCC ACCCTCAGGC AGGAGCTGGT GCTTCCAGT
40501 TGTCACTGAG GTGAGGAACA TATCCAGAA CACAGTCTA AGTGACTAAC
40551 ACTGGAGTGT ATAGTTCTT AGAATTTCA AGTTGGGCA GACTTCAGAC
40601 ATCACCCAGT TACACATT CACAGTTAA CGAATGAATC GAGGCTCAGA
40651 ATAGTAAGT GATTGCGCT GCACCACTCA GCTTGTATG GAGCAGGGAC
40701 TTGTTGATAAT ATTGAAGCAT TTATTGTTGG TTTTTAGAAC GCTGAGTTCT
40751 TTACATGAGT GATATCGTTT GACCATCTG TTTAGTAGTT GGGGAAATG

FIGURE 3L

40801 GTCTCAAAGA GTTTAGTAA CTAGCCACTG AGTGGTAGAG CTGAGGTTGG
40851 AGCCTGGCA TTCAAATCC AGAGCTACA CCCATTCTTA TACCAACCTC
40901 TCCCTGGGC TCAGTCTCC CGATTGTAC CTCACTGAG CTTCCACCCC
40951 ACAGTAACAC CTGGCACCAT CACTGCAAGG ATGACATTAG GCAGGGAGAC
41001 CCAGACCCA GAGAGGGAA GTGTCCTGGT GTCGGTACCA CAGCAGACCA
41051 GCTTTTGT TGAGGCTTAG ATGACCTATG ATGAGAATGC TGTTTGTCA
41101 TCAGCCTACA ATTTCACCTC CAATTTCTC CATATTCAAC CCTCAAGGTT
41151 TGGGGGATGT CACCAACTCT ATTTCAGAACG AGCTAAAGGC TGAAAACATA
41201 GTAGTTTGAG GTTTCAGGGG AATTAAAGC CTAACCTTT TGACACCTTC
41251 TCAAAGCCTT GAGATCGGT AAGATGTTAA TGAGAATTGC CATTATGTT
41301 GATTAAATGA AGAAGGAAAG ATGAGAAGT GCCCCAGAGT ATATAAACACT
41351 GTGGCAGGG TGATGAGCTG ACTCGATATC TTGTAACCC TTTGCTGTCA
41401 GGCTTGGAT CCTTGTCCA ATTTCACCTG ACAAAAGCAGA AAGAGGTCA
41451 GGCTGATCGT GTGCTGGTT CTCCACCATG CACCATGTC CATCCCTGTG
41501 AAAGCTAGGC TGGGTATCA CCTCTCATTT CCTCACAGGC AGGATCCTTC
41551 CACTGATCCG CCAGACTCC TGTCCTCCCT CCCTCTGCAT TTCCCTGCC
41601 ATCAGGCTG TGAGGTTATG GGCCAGGGC TTGAGGTCTC GGATCCTGGT
41651 CCCAGCTCTG TTGCTTCTG TGCTTTACAC CCTCTGGCC TCTCTTCCA
41701 TAGGACTGTA GAAATATTGT GGAGTATCAT ACCTGTGAAA CAGAGGCAGA
41751 TTACACCTCA CTAGTGAATG CTAGCAGTG CTCTCTGCTG GTTACCACTA
41801 GACATTCTG AGTAATGGAA ATGAAATGGA ATGTCCTCATG TGTTGCTGT
41851 CCATTGAGC AGCCACTAGG CACCGTGGT TGTTGAGCCT TTGAAATGTT
41901 GCTAGTGTGA ATGAAAGAAC GGGATTTAAT TCATTTAAAT TCATTTCAAT
41951 GTAAATAGCC GTCCGTTGGCT ATGTTGACCA GCACAGCTCC AGGTAAGTG
42001 TGAGCAGGA GGCATGAATC CATTCTTCC CTGGTGTGTT AGTCCATTG
42051 CGTTGTTATA AAGAAGCACC TGAGACTGG TAATTTATAA AGAAAAGAGG
42101 TTATTTTTGG CTCTGGCTC TGAGGCTGT ACAGGAAGTG TGATGCCAG
42151 ATCTGCTCT GTGAGGGCC TCAGGAAGCT TCTAATCATG GCAGAAAGCA
42201 AAGGGGGAGC AGGCTTTATA TGGAAGACCA GGGAGCAAGG AGAAGGGAGG
42251 TACCGAGCTC TTTAAACAA CAGCTCTCTC AGGGAGGGCC CAAAGTCATT
42301 CATGAGGGAT TTGCCCCAC GACTCAAACA CTCCCACCA GGCCCCACCT
42351 CTGACATTGG GGATCACATT TCAACATGAA ATTGGAGGG GATCCAAACC
42401 ATATTACCTG GTAAGTCTT GTTTCCACAT GTCTCTCATC TTACTGCAGG
42451 GAGTGTATT CTTTTTGTG TGTTTTATG GTCCTCTAAA AATCAACTTT
42501 AGACATTCA GTTTAAAGG TTTCTTTAAA ATCTGGTCTC TAAATGCAAT
42551 CCAATCTTC AGCTGCTCAG CAAAGAACG AGTGATCGAT GTAGACATTG
42601 GTGCTTGGT ACTGAGATG TCTGGCAGTC TCAACAGTGT GGTGCTTCC
42651 TTAGAGTGA TTGACTGCA TTTGCTTCA CAGAATGAA TTAGAACAA
42701 ACCTCTCAT AAAATGTA CCTCTCTGTA GGAATCAATG AGGTAGTAGA
42751 TAAAGCTGG ATGCTGTAT CAAGGCTGG AGCATCCAGC TGAGCCAG
42801 CAGTAGAAA GACAATCTG CAAACTATAT TTGATTGCTA ACAGGTTAGT
42851 AACTAACAGG AAGTCATGCA CTGAGCAGGE ATGTACTTTT CATGGCCAAA
42901 AAAGATGATA CTAATGATGA TAACATTAAC AGGTAAGACA CCTCTACTGT
42951 ACACCAGGCC TTTTGTAGG CACCTGCAAA ACCTCATTTG ACCATCATGA
43001 CATCTCTAT ATTCAAGGAC AGTTAAATTC CCCATTTCG CAACAAGAAA
43051 ACTGGGGAAAT AGAAAAGTAC CATACTTCC CCAATGTCAC TCAGCTAATT
43101 AGCAGCAGG CCAGGATCT AACACAAGAA CCTAGTTCA GAGCCCAAG
43151 GCCTCAATAAA ACCTGTGAAA CACTGGCTT TGCCCACCT GTGAAAAGAT
43201 CGGTGAGATG GGAAGCTGGG GGTCACTGGG CACTAGGATG GTGTATTCTG
43251 GTGAAGCCCT CTCTGCTTA CAGCACTG TGCGACTGTT GACAATGGCT
43301 GGTATGGCAC GGAAGCCGAT GGCACTCTT GGGCAGTGC ACCATTGGTC
43351 TTTCGTCAGTT CCTCTCTCT GGTCACCCCG TGCTGAGTT TCAGATGTGA
43401 GAGCCAGTGG GTGCTCTGC ACAGAGATAC GGTCTGCTG TGGGCTCTG
43451 CCAGGGTCA GCTCTGCAAT AGAACTGCTT TTTTCACCT GTATCAAAT
43501 GCTCTGTGAA ATGCGGTTT ATCACGGTGT CTTTCCAGAA GGCGGGGTT
43551 CTTTCTTAT TTGGTTCTT GTCACTGG TAGAGATGG TGTGTTGGAG
43601 GCTCCCTGAG TGGTAAGAAA ATGAGCAGCT GCTCAGGAC GTCCACCTCC
43651 TTTCCTCTC CCTACCCCTCC CTCCCTGGGT TGCTGAGTT TCAGATGTGA
43701 ATGTAATTG GTTCCCTTTG CACAGAAAATG TGGAACTCAT GTGCTGTAGC
43751 CGGAAAAGT GAAAGCTCTG GGACCGGAGC CAGAAGATCC GGGTTCCGGT
43801 CCCAGCTCTG CTGACCTTGC AGTGGGAAGC CAGTTATTC ATGTTCTGG
43851 GCATCTATT CACAGAGATT GAACCTGACA ATGCTAAGT TTCTTAGAG
43901 CTCTCAATTC TATAAGATGG ACAGATGCTG AATTGCTCA ACAGTAGGGA
43951 GACAGACCTT TCCCAAGATTC TGGGCATCTT AAACAGGCAT GTCCCTCTC
44001 CCTGGCAGCA CCTGGCCAT CTCATCCCC CGCTGGACCC TGTCATCTC
44051 CCTGGTGGGC TCCGTGAGCA GCAGCGCCCT GGCCCTCATC ATCCACCCG
44101 TCCCTGGAGGT CACCACTTC TACTCGAGG GCATGAGCCC CCCTCACCAT
44151 CTTAAGGAC GGCCTGATCA GCATCTGGG TTTCGGGGG TTGTTGGTGG

FIGURE 3M

44201 GGACCTATGA GGCTCTCAT GAGCTGATCC AGCCAAGCAA TGCTCCCAC
 44251 TTCACTAATT CCACCTGTGC CTTCATATAG GGATCTGGGT TCGTCTCTGC
 44301 AGCTGCCAAC CCCTGCCCA TGTACCATTC GGTACCTGTC CTAGAGCCT
 44351 CAGGTATGGT CCAGGCTCTG AGAAAAGTC GGGTTGCTGT GTGGGAACCC
 44401 CTCTGCCCTGG CACCTGGATA CCCCTGGCCCA GGTAACCTGA GGGCAGGGGA
 44451 GAGGTGGGGT GGCAGACACG CAGAAAGTGT ACTAGTGACA GGCTGCCCCAT
 44501 CGCTCACCTG TACCTTTA CACCCAGAAC TTTCCAGCTC CCCCTCATCA
 44551 TGCCCTCTCC TTCCACTGT CCTCCCTCTG GCTGGTGCAC CTGGCCCAAC
 44601 TCATTTCTAC TGACAGCTTC ACTTTTTA ACAATTTCAG TGTCCCCCAC
 44651 CTATGTTT CACCTTTAC TGGGCCAGGC ATAGATTAAG TAATCTGGAA
 44701 CGCCCCCTCT TTATAAGCT GGGCTCTTT CTCATCTCTC TCCCAAATGT
 44751 TGTATCTACTA GTATTCCTTC TATTCGAGTC TCCAGGGGT GGCTGGACCT
 44801 ACCTGGTCAAT TTGAACAGG CCCCCAACGT GGAGTTTTA ATCTGGACTC
 44851 TCTGGCTTGC TGTGACCCCT AAGGAATGTC TTCTCTTCCC TGGTATTCT
 44901 TAGTGTGGGT CACAGTACTG TGTCTTAGT TGCTTTAGCT CTTAAAACAT
 44951 AGCAAGTGTG GCCTTAAACTG AAAATTTA TCTTTTATT AAAATCAGAT
 45001 TTTTGTTTT AGACTGTTCT AGATCTGGGG CTATTACGAA TCACTCTTC
 45051 TTCACTAAAC TTGACTCAA CCTCTCTGCG TGAAAAGAACT CGCTGCCAG
 45101 ATGTCCTCATC GGGTCTCTGG CACTCTGGC TGAGGACTCA AAGGTTTAA
 45151 TCAGGATCGT CTAAAATGT ACCTCGGTG GAGGGCAGAC ATTTCGCTC
 45201 CTGTTGACCA GCCTGGTTTC ATACCGAAAAC GACATTGAAG GACTGAGAA
 45251 ATGATGGGT GCACGGGGC GAGGGAGGG TGGCTGAGTG AGAGGGGTAT
 45301 AAAATGGGGC TGTGTCATG CAGGCCATG TTTCAGCCCTC AGCCCACGCC
 45351 AGGTGGGGAT ATCAGCAATG CTCGTTGCC ATCGTGTGG GAGCACACCA
 45401 GCTCTATTGC CACCGATGAG TAGCTGAGGT CAGTGTGACAG AGAGTTGAA
 45451 ATTAAGTTAA TAGACTTAC AGCAGCTGGT CTGACACTAC GGGCAGTGGT
 45501 CGGTTGTTTA CAATCACTGG GAAAAGGGC AGAACCCAGTC CCGGGCCCCA
 45551 CACTGCCTCT GTGGCCTGGA CTTTGAAGG AACCCACTGA ACACTAATTA
 45601 TGAGGCTCTGT CTTTCCCCCA GAATGCCCTC CTGGGTTCA CAAACAGCT
 45651 TGAGGTTGGC CCTCTCTCAAG GTCACTTCTC AGATTTGGG GCAAACTTCA
 45701 GAGAAGGGCAG AGGAAGATAC ATTGCCCTGC TGTTGGCTGC CTCTCTTTC
 45751 CTCTGGTGT GCGAAGTATT TCAGAAGGGC ATTGATGAT TCCCCCTCTT
 45801 TAGCTGTGA TTTGTGCAGG TGTGTGTTA CGTGCCTGT TGTTGTT
 45851 CCTGTGTAAG TAACAGACCA GACTCTTTT CTCTCTCTC CCGTCACAG
 45901 GCTCTGTGTT CACTGCGAT AGACTTCAC TGTAAAGCTG GTTGAAGGG
 45951 AGCAGAAAAA ATGTATCAGG GTTTTGCTT CTGTGTTTG CCAAAGCTCA
 46001 TAAGGGCTGTG GACCCACCA IATGGGCCCA GTTTTTCTG TCTCTCTGT
 46051 TCCAAAGCCA GGAGAGCTGA CTTCCAGGTG AAAGGGATGGG AAAAGTGGAC
 46101 TCTCATTTGA GTGACTCCCA ACCTACTAA TAATTGTTA ACTTAGGAAT
 46151 ATGCTATCAT TTGTTGACTTG TTCTTCTTA GGAGAAGGAC GATTTTCACC
 46201 CACCCCTTCT GTTCTATGTT GGACTCTTAA CAGGTGCTAT GTGACCGAG
 46251 ATCTAGCCG GAGTAGCAGA GGGCCCTGTCT TCTGAAGTCT CAGGCTTAGA
 46301 AGTTACAAAAT GTGGGCTCAAG AAACCTGTAT CTCCCTGGTC CAAGTTGGG
 46351 CTCTGGCAGC CCAGCGCTA TCTTAACTG TGTTCCAGC GTTGCTAAGA
 46401 GTGGCTCTAG TGAGAAAGTTA GATGCCAACT GGAGGGCAG ACCTGTGTCC
 46451 TGCCCCATGTC CTCCCTGGTG GACGTTTCTG TTTACTCAGA GTGCTAGAG
 46501 ACCATCTCGC CCATCGGAGT TCTGAGATG GGACTGTGAT GTGGGAACCT
 46551 GAGGAATGGG TGTTGAAATA CTGGGGTCCC CCAGCTCTTA GCAGGATGCA
 46601 GGCTATTGCT TCCACACCCCC TGGCCGTGAG AACGTGGTAT GTAGGAGAG

(SEQ ID NO:3)

FEATURES:

Start: 13181
 Exon: 13181-13323
 Intron: 13324-17943
 Exon: 17944-18034
 Intron: 18035-20533
 Exon: 20534-20622
 Intron: 20623-21093
 Exon: 21094-21189
 Intron: 21190-23220
 Exon: 23221-23305
 Intron: 23306-23728
 Exon: 23729-23947
 Intron: 23948-29696
 Exon: 29697-29795
 Intron: 29796-32613
 Exon: 32614-32780

FIGURE 3N

Intron: 32781-35343
 Exon: 35344-35513
 Intron: 35514-44007
 Exon: 44008-44277
 Stop: 44278

CHROMOSOME MAP POSITION:
 Chromosome 5

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain
2064	G	A	Beyond ORF(5')
2119	A	G	Beyond ORF(5')
2121	G	T	Beyond ORF(5')
2123	G	C	Beyond ORF(5')
2125	T	G	Beyond ORF(5')
2825	G	T	Beyond ORF(5')
3288	C	T	Beyond ORF(5')
6172	A	G	Beyond ORF(5')
6462	G	T	Beyond ORF(5')
7031	C	T	Beyond ORF(5')
7671	T	-	Beyond ORF(5')
8466	-	T	Beyond ORF(5')
9097	-	T	Beyond ORF(5')
9108	-	T	Beyond ORF(5')
10170	A	G	Beyond ORF(5')
10966	A	G	Beyond ORF(5')
12987	A	C T	Beyond ORF(5')
13111	C	G	Beyond ORF(5')
13120	C	T	Beyond ORF(5')
13822	C	G	Intron
14891	G	T	Intron
15207	C	T	Intron
16162	G	T	Intron
16364	T	-	Intron
16411	T	C	Intron
16636	T	C	Intron
16802	C	T	Intron
17111	A	G	Intron
17276	T	G	Intron
17372	C	T G	Intron
18317	T	G	Intron
18342	C	T	Intron
21828	C	T	Intron
22674	T	C	Intron
22683	T	C	Intron
22822	C	G	Intron
23073	G	A	Intron
23343	C	-	Intron
23396	T	A	Intron
23511	G	C	Intron
23522	C	G	Intron
23582	T	A	Intron
24977	G	A	Intron
25131	A	-	Intron
25178	G	A	Intron
25351	G	A	Intron
25380	A	G	Intron
26737	G	A	Intron
26829	G	A	Intron
27423	G	A	Intron
27735	G	A	Intron
29875	C	G	Intron
30356	G	T	Intron
31344	C	T	Intron

FIGURE 3O

32570	T	G	Intron
33220	T	C	Intron
33525	T	G	Intron
34589	A	G	Intron
34832	G	T	Intron
35188	A	G	Intron
35614	G	C	Intron
37852	C	A	Intron
38643	G	A	Intron
39198	G	T	Intron
39550	T	G	Intron
42281	A	G	Intron
42321	G	A	Intron
42563	G	C	Intron
42675	G	A	Intron
42908	G	A	Intron
43358	-	G	Intron
43371	G	C	Intron
44796	G	A	Beyond ORF(3')
45820	A	G	Beyond ORF(3')

Context:

DNA Position

2064	CTTCGACTGGACTCTGCCCATGCCAAGATCAATGCCCTGTTAGTCCATTGCACT CCCCAGGCCAGAACATAGTCCTCCAGCAGTCAGTAAAGTCGCCAGGTGGTGC TGTGGAGCAGAGCTCCGAGCTCAGTGAGAAAAAGGCCGGCGCTCAAGGGAGCACGT GACCTCCGGCTTGGCGTGGGATCAGCTGATGAGGTCCGGAAGCGCTGGCG GCAGCAAAGGAGGATGGCAGGGCTGATACTGAACCCGGAAAGGGTGGCTGTGAA [G, A]
2119	CCAGAGCCGGAGCCGGAGCTGGGCCAGAACCCGAGCAGTGAGTCCCACTGACGAGT TCCGGCTGGGGCGCTCGCCGCTTGGCAGGACCCACCTGCCCTCTCCGGCTGGC AGATGTCAGGTGAGGACTGGATCAGCTGGGGCTGGGTCGGGAGACTCTTGGCGTC CCCGGGCAGCTGGTACGCGTACACCCCTGTGAATTGGCGAAGCGTGGAG ATCCCTTGTCCCCTCGCGTATCTCCCTTGACCTCGTGGGGTGGGATCTACCGTCTGT
2121	GCAGTCCCCAGGCCAGAACATAGTCCTCCAGCAGTGGCAGTAATAGTCGCCAGGT GGTGTGGAGCAGAGCTCCGAGCTCAGTGAGAAAAAGGCCGGCGCTCAAGGGAG CACGTGACCTCGGCTCTGGCTGGGGCTGGGATCAGTGATGAGGTCCGGAAGCGCTG GCCGGCAGCAAAGGAGGATGGCGAGGGCTGATACTGAACCCGGAAAGGGTGGCTGTG CTGAAGCCAGGGCAGGGAGCTGGGGCAGAACCCGAGCAGTGAGTCCCACTG [A, G]
2123	CGAGTCCGGCTGGGGCGCTCGCCGCTTGGCAGGACCCACCTGCCCTCTCCGGC GTGGCAAGATGTCAGGTAGGGACTGGATCCGCCCCGGCTGTGGGTCCGGACTCTTG GCGTCCCCGGGCGAGCTGGGTACAGCGCTGACACCCCTGTGAATTGGCGAAGCG TGGAGATCCCTTGTCCCCTCGCGTATCTCCCTTGACCTCGTGGGGTGGGATCTACCGT CCTGTTGACTGACAGGTGGGGAAACTGGGGTAGATGGTGAAGATAACCCAAAGGACATC TGTTGACTGACAGGTGGGGAAACTGGGGTAGATGGTGAAGATAACCCAAAGGACATC

FIGURE 3P

CAGATGCTCCAGGTAGGCACTGGATCCGCCGGGCTGGGTCCGCACTCTGGCGT
 CCCCCGGCCGAGCTGGCTACAGCCTGACACCCCTCTGAATTGGCGAAGCGTGG
 GATCCCTTGTCCCCTCGCGTATCTCCCTGACCTCGGGGTTGGATCTACCGCTCT
 TTTGACTGACAGGTGGGGAAACTGGGTAGATGGTGAAGATAACCAAAGGACCATCTA
 2125 CCCAGGCCAGAACATAGTCCTCCAGCAGTGGCAGTAATAGGTGCCAGGTGGTGT
 GTGGAGCAGAGCTCCGGAGCTCAGTGAAAAGGGCGGCTCAAGGGAGCACGTG
 ACCTGGCCTGG
 CAGCAAGGGAGATGGCGAGGGGGTGTAGATCTGAACCCGGAAAGGGTGGCTGTGAAG
 CCAGAGCGGAGCCGGAGCTGGGGCAGAACCCGAGCAGTGAAGTCCACTGACGAGT
 [T, G]
 CGGGCTGGCGCGCTCGCCGCCCTGGGAGGACCCACCTCGCCTCCCGCGTGGCA
 GATGCTCAGGTCAAGCAGTGGATCCGGCCGGGGCTGGTGGTCCGCACTCTTGGCTCC
 CGGGCCGAGCTGGCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 TCCCTGTCCCCTCGCGCTATCTCCCTGACCTCGGGGTTGGGATCTACCGTCTGT
 TGACTGACAGGTGGGGAAACTGGGTAGATGGTGAAGATAACCAAAGGACCATCTAGG
 2825 AGAAACTGCAAGGACGCTGGGAAGTCGTTGGTCAGCTCCCTCTAGGACAGTTGGAGAA
 ACTGAGCCCTACTCCGGGAAGGGTAAGGGCTTGCCTAAGGGTATCAGGTTAACTC
 GGAGACGGGGAGACTGGCACTAGAAATGCAAAATGTTCTAACGTTCAAGCTCAGGTGTTGCT
 TTTGCCAACACCGCCCTCGGGGAAACTCACCCTGAAAGGCACTCCCTCTGTCC
 TTCTCTTTAGTCCTCCCTTTAGTGTCTGCATTTCCACCGCTGGGTTGGGATT
 [G, T]
 GCTCTGGGTGTGGTCCCTGTTGTCATTATTTCTGAAACTCATCTTCTGTAGGT
 TTGGTTCTAACCTCTGCTTCTATGTAAGTCACACAAAATATGAAATATGAATCGG
 AATGTGCTCTGGGGAGATAGGTGGCTGAGGGAGGGTTGTGAGAGGCGCTGACCTTAAG
 TGAAGAATGAAAGACCTTGTCTTATTCTGTAACTGTGAGATTGGGATTGCTT
 ATTTGGATGGACGTTTGCACTGATTGTAATTGCTGAAGATAGCATATGGTCAATG
 3288 AGAGCCCTGACGTTAACTTGAAGAATGAAAGACCTTGTCTTATTCTGTAACTTG
 TCAGATTTGGGATGGCTTATTTGGATGGACGCTTTGCACTGTTTGAATTGCTGAAGA
 TAGCATCTGGTCAATGGACAGAACAGATGGGGAAATCAGGATATTGCTTAGCT
 CTGGCGCTTACCTGGCAACCTTAAAGTGACTCGCGTTGGGTTCTAGTCTAGACAGTGA
 TGGAAATTGAAATTCTTAAGGGCCCTCTGCTGTGATCTGGATGTGCTCATTTCTAGG
 [C, T]
 TTGTTTTTGTGTTGTTTAAATAGAGATGAGGTCTACTGTCGCCAGGGTG
 ATCTCAACTCTGGGCTCAAGTGACTCTCCACCTGGCCCTCCAAGATTTGGGATTA
 CAGGGGTGAGGGCTGACCTGGGGCTGACGGGTGTTGTTTATTCCGAGGATT
 TACCCGCTGTGACTGAGTATCAGGCTGCAACAAGACTTAACTTAATTGTGAGGAA
 GCAGTTCCCTGTGTTCTGTTGCTATAAAATCTCCCTCTTCTATCT
 6172 GCTTCACAATCCAGAGTTAAATGGAGCCATACTGCAAGACTTGTGAACTTTC
 TCACTTTCTGCTCTGAACTTCTGTGTAATAATCACAATTGCTATCATTAATGGGG
 TTATTATGTCAGGCAACATATCTAACATTATTATTCTCTCTCATCTCATAA
 CAATTTGTGATGTAGATTTAAATGACATCTTCAGATGAGGGAGACTGTGGCAAAGG
 GAGATGAATTAACTGTCTAGACTCACACTACAGACTGCAAACACTGGTCTTTTATT
 [A, G]
 TGCAGAAATACCGCTGAGACCTAACCTGCCAGGCTCTGGGCCAGCTTGTGCA
 GGGAGATTTAAAGGGGTTATAATTAAAGGTGTGAGAAAGAATACTGGACTGGGAT
 GCTGGTTGTGACTGTCTAACATTGTTGATTGACTCATCTGGGCTGGATGA
 GTCAAGCTTGTGTTGGCCCTGTTCTGACCCCTAACAGGAAGCTGGAGCTTGAC
 CTTCTAAAGCTACCTGGCCCTAACATTAGTGTGATCTCATGGTGGAGTAAAAGT
 6462 GCTTTTATTGTCAGAAATACCGCTGAGACCTAACCTGCCAGGCTCTGGGCCAG
 CTGGTTCAGGGAGATTAAAGGGGGTATAATTAAAGGTGTGAGAAAGAATAC
 TGGACTGGGATCTGGTGTGACTGTCTAACATTCTTGTGTTGACTCATCTGG
 GGCCTGGATGAGCTGGCTTGTGTTGGCCCTGGTTCTGACCCCTAACAGGAAGC
 TGGAGCTTGTGACTGTGTTGGGAGTAAACATTAGTGTGATCTCATGGTGT
 [G, T]
 GAGTAAAAGTGTGCGTGGCTGCTGAGCAGCTGCTTGTGAGAAGCTGCTGAGGT
 AGGAGCTGCCCTGTAAGCTGGTCTAGACATCAGACTCTAACAGGAAAAGTCTCAATTATG
 GAATGTTCTGCTGGTAAGTGGATGAAATTCTATCTGATGCTGTTAAAACAAATT
 ATGTTAGAAGCCAAACACTTACTCCCTACTGTAAGGACACATAGCAACACAGTCTG
 TGCTTTGTTGATGTTTAAAGTGGGAGTAAACATCTGGGCTGACAGAGGAGGAAATACATCTGGGAGT
 7031 TCGACAGAGAGGAGAAAATACATCTGGGAATTGGCGCTGCTCTGAGTTCAAAGTCCA
 AACCATGTAATTGTTGAGAATACCGATGACACTTTAGCTGCAAAACAGGGCGCC
 AATGGGTGAATTCTGGTAGGGAGGCTAGGGTGTACCTATCATATAAGATCATAT

FIGURE 3Q

ATTTTTGTAGTCTTATATAAATCTACCTATAATCAAGATTACCTAGGAAGCTAGTTA
 AAAATAAAACGCCCTGGCCTGTAATCCCATACTTGAAGGGCTGAGACAGGGATCC
 [C, T]
 TTGAGGTCAAGAGTTGGACCGAGGCCAACCGGGAAAACTCCATCTCTACTAAAAA
 ACACAAAAAAATTCTGGCCTGTTGAGGCCCTGTAATCCCATCTGGGAGGCT
 GAGGAGGAGAATCTGGCTGAACCCAGGGGGAGGTTGAGTCAGGCAAGATCACCCA
 TTGCACTCCAGGCCGGCAACAGAGGGAGACACCCTCAAAAAAAAAAAAGAACAA
 AAAGACAAAAACAAACAAAAACATAGGCTGGGATGTTGACTCATGCCCTGTAATCC
 7671 TCAAGAGTTGACACCGCCGGCAACATGATGAAACCCGGCTCTACTAAAAATAGAA
 AAAAATAGCAGTTGGCTGGGGCTGGTCTGGTAATCCAGCTACTCGGGAGGCTAAC
 AGGAGAATTGCTGGACACTGGAGGCTGGAGGCTGGAGGCAAGATCGCACCCTGCA
 CTCCAGCTGGCAACAAGAATGAAACTCCATCTCCAGTAATAAATTTAAATAAATAA
 TAAAATAAATAAATAAATGCTAAGGTGGAACTCAAGTGGGATGTTGACTCATTTT
 [T, -]
 TTTCTTGACGTATGTTCATTTAACCCAAATATCCAGATATTATCATTGCAATATA
 TAATCAAGTATAAAAGATTAAATTCATGGGATATTTCACAATTTTGTTACAGTTCA
 TTGAAATCTAGTGTGCACATTCAATTTCACCAAGTGTATTCAAGTGTAAAGTAGCTA
 TTATGCTAGTGGTACTGTACTGGATGTTAACCTTCAGAATATGTTACCATCTATTG
 ATCTTAATCCCTTATTGAAACAAACCCAGTCATAAAATTGAAATTGGAACT
 8466 AAAAAAAACTGTAGAATTCCCCCTAAAAATTGCCACCTCTGAAAAAATTAAACCTAC
 AAATTTTTATTTAAATAAGATAAAATTATTTTTTAAATAAAATTCACT
 TTGACATACATTCCATATTGATCCTGGCACAAGTGTCCACCTGCTCATTTT
 AGTCCCACATCTAAAATGGCATTTTGTAGATTGAAAGGCAACACTGGCTATTATAC
 AGCTAAAACAATAGTACATAAGGAAAAGGAAATGTTAAAGTTGTACACTTAA
 [-, T]
 TTTTTTTTTTTTTGGCCATCAACCTGGAGACTTTTACTCAGTTGCT
 CACTCTCTGAGCTAAATATCTAAATGAGATTGGACTTTGTTCTGTTTGTCT
 CAGTAATCTGAAGGACAAGCTGGCTTCACTCTCACATAGTACAACCCCTATTAGACA
 GTTAACAGGACTATTAAATCTCCATAGGGGGGAACTGGCAATTGGAGCAATAGACT
 TGGCTACAGATTCTACAAAGGGGAGCTAAGGGCACTGGGATGATGCCAGACT
 9097 GCCTTGGTTTCCAAAAGAGCCATAGAAAAGACTCCGGGAGTGGCTTGCCCACTGTC
 GATGCTGAATCTTACATAACTGCTCTGAGAAAGGGCTTTGCTGGATTTTCAAGGG
 ATAAGGAAACAGGTTTCTCCAGGTGATCTGTTCTATTGGAAAGATCTGCTTTGA
 TAGAAAGTTCTCTTACACCTGACAAAATCAGGCTCTTGTACTCTCCACGACTGAT
 CCTCTCTGCTGACTTTGAGGCCCCAAATAACAGTCTAATCCATGTCAGCTTT
 [-, T]
 TTTTTTTTTGGAGAGCGGACTCTGCTCTGTCGCCCAAGGCTGGAGTGAGCTGGC
 GATCTGGCTCACTGCAAGCTCCGCCCTCCGGGTTCAACCAATTCTGCTCAGCCTC
 CGAGTAGCTGGACTACAGGCGCCGCTACACGCCGGCTAATTGTTGATTTTCA
 TAGAGAGGCTTTAAAGACAGTTTGTACCCCTCAAGTGTCTAGGGAAACCTTCTCA
 GTGCTTCAACCAATTCTCATTTAGTTGTTTCTACCCCTTGTACTCTAGTCTGACC
 9108 CAAAAAGAGCCATAGAAAAGACTCCGGGAGTGGCTTGCCCACTGTCAGTTGAA
 CCTTACATAACTGCTCTGAGAAAGGGCTTTGCTGGATTTTCAAGGATAAGGAAACA
 GGCTTCTCCAGGTGATCTGTTCTATTGGAAAGATCTGCTTTGATAGAAAAGTTCT
 TCCTTACACCTGACAAAATCAGGCTCTTGTACTCTCCACGACTGATCTGCCCTGC
 CTGACTTTGAGGCCCCAAATAACAGTCTAATCCATGTCAGCTTTTCT
 [-, T]
 TTTGAGAGCGGAGTCTGCTCTGTCGCCCAAGGCTGGAGTGAGCTGGCGATCTGGCTC
 ACTGCAAGCTCCGCCCTCCGGGTTCAACCAATTCTGCTCAGCTCCAGTAGCTG
 GGACTACAGGCGCCGCTACACGCCGGCTAATTGTTGATTTTGTAGTAGAGACGGCT
 TTAAAGACAGTTTGTACCCCTCAAGTGTCTAGGGAAACCTTCTAGTGTCTTCAAC
 CATCTCATTTAGTTGTTTCTACCCCTTGTACTCTAGTCTGACCCCTGGATATAC
 10170 TATACACAAACATAAAAGAAGTCTCTGCACTGTTGAGATAATTGAAACATGTCACAA
 GTAGACAAGAGAGGTTCTGGCTCTAGGGAAAGATTGGCAATTAAAGTCCCTG
 TATTCATCTTACCTTCACTTCAAGTATAATAGGTGTCACCTAAAGGAAGAAGTTGAGAC
 ACAAAATGCAATTTTAACAGTTTACTTGAACTGTTACTTGAACCAAGTGGAGGACAGT
 GCCCGGGACACTTCAAGTGTCTGGGGAGTGGCTTCTGGCTTACAG
 [A, G]
 TTCTTAAGGCAAAGCGAACAGGAGGAGCTGATACAAAGTGTACTGACAGGAATTCT
 CATCAGTTTACAGAAATGAGTGGATTATGATGGCTGACATTGTTGACTATAGGGT
 ATGAGTTATGATGTCAGTGTAGTCAAGGAGTAAATTAACTCAAGGGGGAGTGGACATGAC
 CCACATAGCAAGTGTCTGGGGAGTGGCTTCTGGCTTACAG
 TGCTCTACATTAGTGTCTCTGGGACCGTAAATTAAAGGATTCTCAGATAAAA

FIGURE 3R

10966 CAGGTGAGACACTGCACTCAGCTGCTTTGCATAAATTAATTATGTCATTGACACCT
 AGAATATTAGTGTAGGGAGGTGAGAGATATTAGTTATGCCCATGTTTGC
 CATTGAAATGGTCAAGTACTAACAGCAAATCTGAACTGTCAGAGGTAGGCTGGCCCTG
 GGCTCTGACATACCTGAAACTGATTACAGCTTACCTGTATAGCAAGAGGTTAC
 AATCTGTTAAGAGACTTCAGAGATTTTTCTCCGCCCTAGTGAGTTA
 [A, G]
 TTGCCCCAGCTGGTGGCCTTGAATTCTCTAGTCATGAGTAATGAAGCTCTC
 ATAGATTTAGGCAAGTGGCTCGCAATGAAGTAGGCTCAGGATCTGGGATTT
 CAGGTCTTGTGCAATTGCGAGGTACTCCCTGTGAGATAGCTGGGGTCTTC
 CTACATTGCAATTGAGAGAAAATGGATCTCCGGATCTCTGTGCGAGACTG
 GGGTTTCAAAGGAGTACCCGGCACTGGACCTAAGGAGAGCTGGGAGGACCA
 12987 GTGTATATACGTATATATATATATGGATGATTATATATATATACAG
 CAGCACGATTGAATGGCAAGGTCAGAACATTTCTCAGAAAGGAGTAGATAATC
 CTGACCTAAGGAAATAGGGAAATGGCAATTCTGGAGACTCTCTCTTCTTCCCA
 CTCTCCAAGCAGTGCCTACTCTGCCTGTCACTGACTCTGGAAAATTAAGAAA
 TTATGAGTGTAGCACACGTACCAATGGAGGGATGGAGTCAGAAGTCAGTGAAC
 [A, C, T]
 CAGCCCCCTCTGTGACTTTGCACTTCCCCTGGTACAGGCACTTCACAC
 TTAATCATAGTGGACATGGCAACTCTGGAGACTCTGACAATGCACTCTACCCAGA
 GGCCACCCAAAATGGAGCTAAAGCTCAGTCGAGGAGTCTTAATGTCGGCTGT
 CCCCGAGCTGCGATGTCCAGCAGAGACTTCGAAGATGAAGACTACACGACTACAGCTC
 CACGGACGTGAGCCCTGAGGAGAGCCCTGGAGGGCTCAACACCTCTCCCGGG
 13111 CCTAAGGAATAGGGAATGGCAATTCCAGGAAGGACTCTCTTCACTTCCCCACTCC
 TCCAGGAGCTGCTCCTCTGGTCACTGAGGAGGATGGGAGTCAGAAGTCAGTGAACCTAG
 TGAGTGTAGCACACGTACCAATGGAGGATGGGAGTCAGAAGTCAGTGAACCTAG
 CCCGCTCTGTGACTTTGCACTTCCCTTGTGAGGACCTTCACAGGCACTTCACTTA
 ATCCATAGTGGAGCTGTCACAGTGAGCAACTCTGACAATGACAGCTTACCCAGAGGC
 [C, G]
 ACCCCAAAATGGAGCTCAAGGCTCAGTCAGGGAGGCTTAATGTCGCCCTGTCCCC
 CCAGCTGCCATGTCACCGAGACTTCGAAGTAAGACTACACGACTACAGCTCCAG
 GACGTGAGCCCTGGAGGAGGCCCTGGAGGCTCAACACCTCTCTCCCGGGCTCC
 TACAGCGTTGGTCAAAGCAATGACACAAGTGAGTAGCTGTTACCTCTCTCT
 GGGTGGGATTGTTCTAAGCTCCCTGGACTTATTTCCCCCAATTTCATCAGT
 13120 TAGGGAAATGGCAATTCCAGGAAAGGACTCTCTTCACTTCCCCACTCTCCAAGCA
 GTGCCACTCTGCTCTGTCACTGAGGACTCTGGAAAGGATGGGAGTCAGAAGTCAGTGAACCTAGGCCCT
 CACCACTATACCAATGGAGGATGGGAGTCAGAAGTCAGTGAACCTAGCTCT
 GTGACTTTGCACTTCCATTCCCTGGTACCCGGACTCTTCACTTACATTAATCAGT
 GGAGCTGTCACAGTGAGCAACTCTGACAATGAGCTTACCCAGAGGCCACCCAAA
 [C, T]
 ATGGAGCTAAAGGCTCAGTCAGGGAGGCTTAATGTCGCCCTGTCCCCCAGCTGCC
 ATGTCACCGAGACTTCGAATGAAGACTACACGACTACAGCTCACGGACGTGAGC
 CCTGAGGAGGCCCTGGAGGCTCAACACCTCTCTCCCGGGCTCCACAGCGC
 TTTGGTCAAGCAATGACACAAGTGAGTAGCTGTTACCTCTCTCTGGGTGGGAT
 TCCTGTTCTAAGCTCCCTGGACTTATTTCCCCCAATTTCATCAGTCTCCACTT
 13822 TCTCAGCTGTTGGCCCCCAAGGCTGTGCAAGTGGAGAGCTGGACTAAAAAGCT
 TCTACAGAGGACATTCTTAAATTAAAAGTGTGATCTGTGCTAGAACCCAAAATAT
 TTCCAAAGCATATCGGAAGCTCCCTTGAAGCTTCCGGGAATTTGCCCCATCACC
 AAATCAGTATTCTTGTGACTGAAGAGTGGAGAGAGAAGAATTAACTCTGCACTTAA
 AAAATTCAGGGTTGGTAGGAAGGAAAGATAGACTTGTGATTCTCCAAAGAGGGCTTAA
 [C, G]
 TCTGTCTCGAAAGAACCTGGAGCCCAAGACTCTGGCTGAGTTGGCCCTTCAGGT
 CTCACTTCCCCAAATGAAAGAAAATTGAGGACTCCACCAAAAGCTATGTCGGCTGT
 GTGGGCTCACCACTGAAATTAGGAAATTCAAGGAGGTTGGTCACTCCATTGAGTTAG
 TTCTCCAGCTACTCTGATTTCAAGCAGACCTCTGACTTTCTGTGTCAGCATCTA
 GCTTTGCACTGTTTATTCTCAAGCTTAGCTTACCTTTCTGTGTTCTGTG
 14891 GAGGTCTGTTATGTAAGATACCTCTAAGCTCTCTCTGAGTTCCCTTGC
 GTTTTGCTCTTTGATCTCAGATATCAACTGTCAAGAAATTAGCAGATGAGG
 TCTGGATTTTATGTTATAGAGACATCTCTGAAGCTCAAACCTACCAACTAGCAACTT
 TAGGATAGTAGCTAGGCTAGGTTGGAGAAAATTATGCTCTGTGTTCTGGAAATCGAAC
 AATCAGAAGATACCTCTCAGCTGTGATTGTGACATTTCAGGGTATCTGGTCC
 [G, T]
 AGTTCCCTCTGGCTTGATGTTGATACAGTGTAGGTGACCAAGGGATCTGT

FIGURE 3S

AGTTGATGGCAGGTATTACAGTCCCACAGGTGGTACAAGATAAAAGTAATTGCTGGG
 GCTTAGAGGACTGGTGAAGTCTCCAGGGCATAGGATCCACCGAAGGATTATA
 TAAAGAACATGCCAGGTATTAAGGTAGAGGTTAGTTGGAGGACCTTCAACCTAA
 ATTAATTTAATATGTCGGAAGTGTAGAGACAAGTTTGAGCTGGGTTCTTTAT
 15207 CTTGATGTTGATACAGTGTAGGTGACCAGGGAGCCTATCTGAGTGTGGCAGGT
 TTACAGTCCCACAGGTGGTACAAGATAAAAGTAATTGCTGGGCTTAGAGGACTGGT
 TGAGTACTCCAGCTGGGCATAGGATCCACCGAAGGATTATAAGAAAATGCCAG
 GTATGATTAAAGGTAGAGGTTAGTTGGAGGACCTTCAACCTAAATTAATTTAATA
 TGTCGGAAGTGTAGAGACAAGTTTGAGCTGGGTTCTTTATTTCTGGTTGCC
 [C, T]
 ACCCTTTATCTAGTTGGCAAGGAACAAATACATGGAAGTACTCTACACCTACTGC
 ACATATGCATGCACACACCTGGCTCTTAGCAAGTCAGGGCTCAGAAAAACCCCTAG
 TTAGGGGTCAAATGGAAACCCCCAACACTCCATAGGTTCATGGGTTACTCTTT
 TTTAGGGTGAAGACAGGGTCTGGCTCTGGTCCAGGTTGGAGTGCATGGCACATCG
 ATTTTGTAGGACAGGGTCTGGCTCTGGTCCAGGTTGGAGTGCATGGCACATCG
 GTCACTGCACCTCCATCTCTGGCTCAAGTGATCTCCACCTTAGTTCTAAGTA
 16162 GCAGACTGAAACTGGCTCTAAAGGTAGGCTGGAGTAGTCATTGCAAAATGTGGCTG
 CACACTTTGGGCTTCCAAGACCAATTCAAGAAAGTCTAGGGCTAAAACCTCTTC
 TAATAATACTAAAGATGTCTCTGCTTCACTTGTGAGTATTGCACTTATAATGAGA
 AGCAATGGGGTAAATTACACTGTAGAACGAATCAAGGAGTGGCACCAATTAACT
 AGTTGCTGTATTTCACTGCCACATGCGCAAAGAAAAAGCCCTTGCACCTAA
 [G, T]
 AATGCTTGTGAAACTGTAGGATTACTAATATTTAAAATTGAGACCCCTCAGTATA
 GGTTTAAATTCTGTGGCAAATGGGAAGTGTGATGAAGTACTTCTATGAGTAC
 AAAATGTTACTTGTGAGGAAACCTCAGTGGATTATATGAGTTGCAACCAA
 AGTTGCTGTATTTTCAAGAACATAGAAAACAACTAACAAACTGTAGGTCA
 TTGAGCCGGAGTACTTGTAGACATTCTGAAATGAAAGAACATGCCACCT
 16364 CTGAGAACGAATCAAGGCAGTGGCACCAATTATACTAGTTGCTGTATTTCACT
 GCCACACATGCGCAAAGAAAAAGCCCTTGCACCTGAAGAATGTCTTGTGAAACTGTA
 GGATTAAATTTCTGTGGCAAATGGGAAGTGTGATGAAGTACTTCTATGAGTAC
 CAAAATGGGAAGTGTGATGAAGTACTTCTATGAGTACCAAAATATGTTACTGTCTAA
 GGCAAAACCTCAGTGGATTATATGAGTTGTCACCAAAACTTGTGCTCTTTTT
 [T, -]
 CATAGAACTAGAAAGAACAACTAACAAACTGTAGGTCTTCAGACCCGAGTACTTGTAA
 ACATTICCTGAAAGAACAACTAACCCATCACCTCAAGGAAAACAACTAGATAATAC
 ATATCTGTGCCCAGAACAAATTCAAGCTTCAAGGAAAATTAGGAAAAAAACCAACT
 TGTATTCAGTACCATGAGCTTGTAGGCCCTACTTGAAGACTTTCTGATGAGATTAG
 TGGTGTATTAACAATATGACTTTGTATTTATTAATACATGAAGATGTTAACAT
 16411 TGATTTTCACTGCCACACATGCGCAAAGAAAAAGCCCTTGCACCTAACAGTGTCTT
 TGATGAAACTGTAGGATTACTAATTTAAAATTGAGACCTTCTAGTATAGGTCTTTA
 ATATCTGTGTCAGGAAATGGGAAGTGTGATGAAGTACTTCTATGAGTACCAAAATATG
 TTACTTCTTAAAGGCAAGACCTCAGTGGATTATATGAGTTGTCACCAAAACTTGTG
 CTCTTTTTTCTATAGAACATAGAAAAGAACAACTAACAAACTGTAGGTCTTCAAGACC
 [T, C]
 GAGTACTTGTAGACATTCTGAAATGAAAGAATCAGCCCATCACCTCAAGGAAAA
 CAATAGATAATACATCTGTGCCCAGAACAACTTCAAGCTTCAAGCAAAATTAGGA
 AAAATGAAACCTTGTGATCACTGAGCTTGTAGGCCCTACTTGAAGACTTT
 CTGATGAGATTAGTGGTGTATTAACAATATGACTTTGTGATTTATTAATACATGA
 AAGATGTTAACATTGGAGATCTGTGAACTAACCAAGTGTAGTTGAGATTCT
 16636 AACCAAACCTGTGCTCTTTTTTCTATAGAACATAGAAAAGAACAACTAACAAACTG
 TAGGTCTTCAAGACCCAGTACTGTAGGACATTCTTCTGAAATGAAAGAACATGCC
 ATCACCTCAAGGAAAACAACTAACATGATGAAACTATCTGTGCCCAGAACAAATTCAAGCTT
 TCAACCAAATAGGAAAAAAACCAACTTGTATCAGTACCATGAGCTTGTAGGCCCT
 CTACTTGAAGACTTTCTGTGAGATTAGTGGTGTATTAACAAATATGACTTTGATA
 [T, C]
 TATTAATATACAATGAAGATGTTAACATTGGAGACTGTGTAACACTAACCAAAGTAT
 GATGTTAGGAATTCTGTGATGGGAAAAGATCCATTGAAAGAGCAAGATCACCATGGATT
 TTTTTCTTTTTGAGACAGTCTGTGCTGTGACCCAGGCTGGAGTGCAGTGGC
 ACAATTTGGCTCACTGCAACCTCTGCCCTCCGGATTCAAGCGATTCTGTGCTCAGCC
 TCCCGAGTAGCTGGGATTACAGGTGCTGCCACCACTCCAGCTTAATTATTTA
 16802 TAAAATTCAAGCAAATAGGAAAAAAACCAACTTGTATCCAGTACCATGA
 GCTGTGATAGGCCCTACTTGAAGACTTCTGTGAGATTAGTGGTGTATTAACAAAT
 ATGACTTTGTATTTATTAATACATGAAGATGTTAACATTGGAGATCTGTGTA

FIGURE 3T

ACTCAACCAAAGTATGATGTTAGGAATTCTGCATGGTAAAGATCCATTGAAAGGCAA
 GATCACCATGGTTTTTTCTTTTTTTGAGACAGTCCTGCTCTGTACCCAGG
 [C, T]
 TGGAGTGCAGTGGCACAATCTGGCTCACTGCACCTCTGCCCTCCGGATTCAAGCGATT
 CTTCTGCCTCAGGGGGCTGGGAGTAGCTGGGATTACAGGTGCGCCACACTCCAGCTAA
 TTTTATTTTATTTAGAGACGGGGTTTCGCCTGGGAGTAGTCTCAATCTCTGACCTA
 TGACCTCATGATCTGCCGCCCTGGCTCCAAAGTGCTGGGATTACAGGCATGAGCCAC
 TGACCTGGCTGACTTTTTTTAAATACTAAATGATCAGGGACTTCTGGCT
 17111 AGTGGCACAATCTGGCTCACTGCACCTCTGCCCTCCGGATTCAAGCGATTCTCTGCC
 TCAGGCTGGGAGTAGCTGGGATTACAGGTGCGCCACACTCCAGCTAAATTTTATA
 TTTTATTTAGAGACGGGGTTTCGCCTGGGAGTAGTCTCAATCTCTGACCTA
 TGATCTGCCGCCCTGGCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACCTG
 GCCTGACTTTTTTTAAATACTAAATGATCAGGGACTTCTGGCTCTTATGGT
 [A, G]
 TGGTGTGACTTTTATGCTGTTCACTTTGTTATCTTCTGTTACAGGGTTGGGCTTCTGT
 TATTATTTATTTATTTAATTTCTGTTCTTACAGTGTGTTCTTACAGTGTGTTCTGCTT
 TTGGTTGTCATCTGCTGGCAGTTGGGATCTGAGTCCTTTTTTTGAGATGG
 AGTCTCCTCTATTGCTTAGGGTGGAGTACAGTGGCAGCATCTAACACTGCAACCTC
 TGCTCCGGGTTCAAGCAATCTCTACCTTAACCTCTGAGAAGCTGGGATTACAGGC
 17276 AATCTCTGACCTCATGATCTGCCGCCCTGGCTCCAAAGTGCTGGGATTACAGGCAT
 GAGCCACTGCACTCTGGCTGACTTTTTTTAAATACTAAATGATCAGGGACTT
 CTGCGCTTATGGTGGTGTGACTTTTATGCTGTTCACTTTGTTATCTTCTGTTACAG
 GGTTGGGGCTTCTGTTATTATTTATTTAATTTCTCTGTTCTTACAGT
 GTGGTGGCTGATTTGGTTGTCATCTGCTGGCAGTTGGGATCTGAGTCCTT
 [T, G]
 TTTTTGGAGATGGAGTCTGCCCTTATGGCTAGGGTGGAGTACAGTGGCAGATCTTA
 ACTACTGCAACCTCTGCCCTCCGGGTTCAAGCAATCTCTACCTTAACCTCTGAGAA
 GCTGGGATTACAGGCACATGCCCTATGCCCTGGCTAATTTCTGTTATTTTAGAGAGG
 GGGTTGCGCTTGTGGCCAGGCTGGCTGCAACTCTGACCTCAGGTGATCCACCGCTT
 CGGCTCCAAAGTAGTGGGATTATAGGCATGAGGCACATGCTGCCAGGCTGAGCC
 17372 AAATACTAAATGATCAGGGACTCTGGCTCTTATGGTGGGTGACTTTTATGCTGT
 TCACTTTGTATCTTCTGTTACAGGGTTGGGCTTCTGTTATTATTTATTTT
 AATTCTCTGTTCTTACAGTGTGGGTTGCTGCTCATGTTGGTTGTCATCTCTGTT
 GCAGTTGGGATCTGAGTCCTTTTTTGAGATGGAGTCTCCCTTATGGCTAG
 GCTGGAGTACAGTGGCAGCATCTAACACTGCAACCTCTGCCCTCCGGGTTCAAGCAA
 [C, T]
 TCTCCTACCTTAACCTCTGAGAAGCTGGGATTACAGGCACATGCCCTATGCCCTGGCTA
 ATTCTGTTATTTTAGAGACGGGGTTTCGCCTTGGCAGGCTGGTCTGCAACTC
 CTGACCTCAGGTGATCCACCGCTCGGCCCTCCAAAGTAGTGGGATTATAGGCATGAGCC
 ACTGTGGCTGGCCAGGCTGGCTTACAGTGGCAGTCTGTTAGAACCAGACCC
 AAATACACTTGGAAAGGATAGGTCTGAAGAGATGGAGCACCCCTGGCTTAATC
 18317 AAAATGCAGGCATCTGGTAAGGGCTGCATCAGTGGAGAGGAGTGGTACAATTTA
 GGAGGTGCTTGTGTTAAAATGACTGCTTAAAACATTAAATAGAGAAAG
 CATTAAAAAAATCAGTGCACAAAAGCGAATTGACAGCATCTTACCTAAAGAT
 TATTAGAGATGTTCTGCTGGTACGGACTGTTCACTGAGTCTTAACTGAGAT
 TAATATTCTGCCCTCATGGAGCTTACGGAGGATGTACTGAGATGGCT
 [T, G]
 AGCAGTCTGCAATAATATGAACATAATGAGTTAGTACAGATGTCCTGCTTCTA
 CAGTCTCCATGCCCTTCTCAAATGGCAACTGCAAGAATCTTATGCTCTTCTG
 GATTACCTCCAGTGAETGCCCTGGCTCCAAAGGCATCTGGTTCTGGAGTTGAAGAG
 AGACTCAGAGATGGGTTGGCTTACAGTGCAGTCTTCTGATCTGGCATTGCTG
 TAAGATAACTTACCCGCTCTACCTCATGGAGGAGGATGTACTGAGATGGCT
 18342 TCTGCATCAGTGGAGAGGAGTGGTACAATTTAGGAGTAGCTTTTGTGTTAA
 AATGACTGCTTAAACATTTAAATAGAGAAGCATTTAAAAAAATCAGTGCACAA
 AAGCGGAATTGAGACATTCTTACCTAAAGATATTAGAGAGTGTCTGCTGCTTAG
 GCACTGTTCTAAGCTTAAAGAATACATGAGTCACTGAGTCTTCTGATCTGGAGCT
 TACTTCTGAGGAGGATGTACTGAGATGCTCGAGCAGTTCTGCAATAATATGAA
 [C, T]
 TAATGAGTTAGTACAGATGTCCTGCTTACAGTCTCCATGCCCTGTTCTAA
 TGGCAACTGCAAGAATCTTATGCTCTTGTGATTACCTCCAGTTGACTGCTGC
 CCAAGCCATTCTGGTTCTTCCGGAGTAGAGAGACTCAGAGATGTGGGTTGCCCTT
 AGCTAAGTGCAGTCTTCTGATCTGGCATTGTAAGAGATAACTTACCCGCTCACCT
 CACATCCCTAGCCAGCTTCCCAACAGTCACAGGAGGCTCTATTCTGATGTGCA

FIGURE 3U

21828 AACAGTTCTAGGTAAAGAAGGGAAAGATTTCTCTGAAGTAAATTATGTGGTCTTACCCCTCA
 GAGGCTTGATGTCTGTAAAGGAAAAAGAAATGTGGAAAGAGCAGGGAAACAAGATA
 AGACGAGCATGTGGAGACCCATAAAGAAGAAAGTGTATGAGCTAGGAGTACACCCCT
 CAGTGCTCAGAGAGAGGAACTTAAAGATTTCTCTTGCGCTGTGCCAGATGAGAAC
 GCACATGAGAGATAGGAGCAAAGAAGGCTTCAGGAGAAGGTGAGATAAACTAGAGCAGGG
 [C, -]
 GTGGAGATGAGTTGGAGGTGGAAAGTAACTTCTCGTTATGTAACCTTCA
 TGTTTGGAGGGAACTTATGTTGTTCTACATTAAATGAGGAATTGATACTATC
 AAGGGCTAAAAAATCTTAAAGGAAACCACTAAAAACTATGTTCTAGA
 AAAGTTCTTTTGTGTATAGGAGGAACTTACTTCTTCACTAGTCACCTTATCTG
 TGATGAGATTATAGTGTCTTGCCAAATTATCTGTAACTGGAGAAGCTAGAT

22674 CATACACATGTTCTAAAGTTTGCACAGATTGACCATACATGTATACGTGTTGAA
 ACTTGTCTTCTTAAACGCTGTAGACGCTTTCTATCAGCACATAGAGATTAA
 CACATTCTTAACTGCTGTAAATGTTCCATTAAAGAACGGTCTATAAATTAACT
 CTGCTTTGATGATCTTAACTGTTGACCGCTGTATGTTCAACCCAGCTGT
 TTGGTACATCAGTTCTGTCTTAAATGTTGGACTTGGTCTTATATCCAAGTT
 [T, C]
 AGAGACAGTGAAGGGGACTATTCTCTGTGTTATGTCAGGGCTCCCTGTAACTAAC
 AAAAGATGTGAGATGGGAGTAGGTGGCAGATGTGAGAGGAGTGTCAAGGGCTGGGCA
 GTGGTCTGGTCTGTGCTGTCTCACCTCATGCAAGCATTCCAGACGAGAACGCCAG
 AAGGGGAGCTCGAAACACAGATAGCACCTCCACCTTCCCAATGCCCAAG
 CCAGTGGCACCTAGCATGGTTCTCTCTGGCAGGGCATCTGCTTGTACTGCCAG
 22683 GTTCTTAAAGTTTGTGACAGATTGACCATACATGTATACGTGTTGAAACTTGT
 TCCCCCTAAACGCTGTAGACGCTTTCTATCAGCACATAGAGATTAAACATTCTT
 TTAACTCTGTGTAATGTTCCATTAAAGAACGGTCTATAAATTAACTCTGCTTTG
 ATGATCTTAACTGTTGACCGCTGTATGTTCAACAGCAGCTGT
 CAGTTCTGTCTTAAATGTTGGACTTGGTCTTATATCCAAGTTAGAGACAG
 [T, C]
 GAAGGGGACTATTCTCTGTGTTATGTCAGGGCTCCCTGTAACTAACAAAAAGTG
 GAGATGGGATAGGTGGCAGATGTGAGAGGAGTGTCAAGGGCTGGCAGTGGTCTG
 GTGCTGTGCTGTCTCACCTCATGCAAGCATTCCAGACGAGAACGCCAGGGAC
 TCGGAAACACACAGATAGCACCTCCACCTTCCCAATGCCCAAGCAGCTGCCA
 CCTAGCATGGTTCTCTCTGGCAGGGCATCTGCTTGTACTGCCAGGAAGGGCT
 22822 TCCATTAAAGAACGGCTATAATTAACTCTGCTTTGATGATCCTTGTGTT
 CCAGCTGTATTGTCACCCAGCAGCTGTTTGTGACATCAGTTCTGTTGCTTAA
 GTGGACTTGGTTGGTCTTATATCCAACTTATAGGACAGTGAAGGGACTATTCTT
 GTGTTTATGTCAGGGCTCCCTGTAACAAACAAAAGTGTGAGATGGGATAGTGGC
 AGATGTTAGAGGGATGCTAAGGGGCTGGCAGTGGTCTGTGCTATGTT
 [C, G]
 ACCTCTGAGCATTCCAGACGAGAACCCAGGAAGGGGACGTCGGAAACACAGATAG
 CACCTCCCTCACCTTCTCCAAATGCCCAAGACCAGTGGCACCTAGCATGGTTCTCTC
 CTGCCAGGGCATCTGCTTGTCACTGCCAGGAAGGGCTGTGATGGCTGGGAAAG
 CACTGTTAAAACAACTTAAATGGGACAATGCACTGTGACTTGGGTGACTAA
 ACGCCCAAGGCACTACCATGCTATCCATTAAACAAACAGCACTGTACTCCCT
 23073 GAGGATGCTAAGGGCTGGGCACTGGTCTGTGCTGTGCACTGGTCTCACCTCATGCA
 GCATTCAGCAGAGCAGGGCAAGGGGACGTCGGAAACACAGATAGCACCTCC
 ACCTTCTCCCAATGCCCAAGACCAGTGGCACCTAGCATGGTTCTCTGCCAGGGC
 ATCTGCTCTGTGCACTGCCAGGAAGGGCTGTGATGGCTGGGAAAGCACTGTTAA
 AAAACACTTAAATGGGCAATGCACTGTGACTTGGGTGACTAAACGCCAGGC
 [G, A]
 CTACCACTATGCACTATCCATTAAACAAACAGCACTGTACTCCCTAAATCTTAA
 AAAACAAAACAAAACACCTCCCTCTGGGAGCATTGCACTTGTGTTGAAACAGTCT
 TTGTATTCTCTCCCTCCACCTGCCAGAGCTGTGTTGACTTCTCTGATTGTCACCCA
 GTGGGATTCTGCTGTCTATTGTTGTTCTGGCTGACAACTTAAACAGGTAGGCA
 CTGGTAAAAAAAGAAAAAAACAGAGCAGGAATGGCAAAAGATGATTGAAG
 23343 TTGGGTGATGGGTAACATAACGCCAGGCACTACCACTATGCACTATCCATTAAACA
 AAAACAGCACTGTACTCCCTAAATCTTAAACAAACAAAACAAAACACCTCCCTC
 TGGGAGCATGCTTGTGTTGAAACAGTCTTGTGTTGACTTCTCTCCACCTGCCAGAC
 GTGGTGTGGACTTCTCTGCTGTTGCACTGCCAGTGGGATTCTGCTGTCTATTGTT
 TCTGGCTGACAACCTTAAACAGGTAGGCACTGGTAAAAAGAAAAAA
 [C, -]
 CAGAGCAGGAATGGCAAAAGATGATTGAAGTTTGTGTTAGGATTCTCCAAATCAGCT

FIGURE 3V

TTTGTCAACAAAAGAGTTAAAGTTTATTTACATAGATCTACGTCTTCTATTGAT
 TCCCAGTGGAAAGAGCTGGGCATAGAGAACCCGCCACATGGCTTGTGACCCCTCTGTCC
 TAGTACATATGCAAAACCTAGTCAGAACATTGGTTGCTGTGATGATAGCTGAAGTT
 CTCTAAAGATGGCTACTGGGCCACAGATTCTAAAGGCCCTGTTACACACCTGAGCCTT
 23396 TTTAACAAAACAGCACTTGTACTCCCTAAATCTATTAAAAAACAAAAACAAAAACACCT
 CCCCCCTGGGAGCATTTGATTGTAAACAGTCTTGTATTCCTCCCTCCCCACC
 TCCAGACGTGTTGGACTCTCTCTGTGTTGCTACCCAGCTGGGATCTGGCTGTGCTAT
 TTGTTGTTCTGGCTGCAACACTTAAACAGTGGACCTGGGACTCTGGTAAAAAGAAAAAAA
 AAAAAGAACAGAGCGAGAACATGGCAAGATGATTGAAGTTTGTAGGATTTTCCA
 [T, A]
 ATCAGCTTTGTCACAAAAGAGTTAAAGTTTATTTACATAGATCTACGTCTTCT
 ATTGATTCCCATGGAAAGAGCTGGGCATAGAGAACCCGCCACATGTCTTGCGACCC
 CCTGTCTTAGTACATATGATCAAAACCTAGTCAGAACATTGGTTGCTGTGATGATGCG
 TAAGGTTCTCTAAAGATGGCTACTGGGCCACAGATTCTAAAGGCCCTGTTACACACCT
 GAGCCTTCTCAGAACCTCTTCAGCAGAGGATCCACCGCCCTGTGTTGAGGAG
 23511 CCACCTCCAGACGTGTTGGACTCTCTCTGATTGTCACCCAGCTGGGATTCTGCTGTG
 TCTATTGTTGTTCTGGCTGACAACCTTAAACAGGTTAGGCACCTGGTAAAAAGAAAA
 AAAAAGAACAGAGCGAGAACATGGCAAAGATGATTGAAGTTTGTAGGATTTT
 TTCCAACTGAGCTTGTCAACAAAGGTTCAAGATGGCTACTGGCACAGATTCTAAAGGCCCTGTTCA
 TCTTCTATTGATTCCATGGAAAGAGCTGGGATAGAGAACCCGCCACATGTCTTG
 [G, C]
 ACCCTCTGTCTTAGTACATATGATCAAAACCTAGCTAGACAATTGGTTGCTGTGATGAT
 AGTCGTGAAGTTCTCTAAAGATGGCTACTGGCACAGATTCTAAAGGCCCTGTTCA
 CACCTGAGCCTTCAGGAACCTTCCAGCAGAGGATCCACGGGCTCTGTTGTTG
 AGAGGTTCTGGTTCTCCCTCCTATTCTAGGTGATAGAAGGCCCAATGGAC
 CACCAATACTGCCAACAACTGAGACGGTATTCTGAGCCTACCATGGACTCGGACT
 23522 CGTGTGTGGACTCTCTCTGATTGTCACCCAGCTGGGATTCTGCTGTGTTATTGTTG
 TTCTGGCTGACAACCTTAAACAGGTTAGGCACCTGGTAAAAAGAAAAAAA
 ACCAGAGCGAGAACATGGCAAAGATGATTGAAGTTTGTAGGATTTTCTAAATCAG
 TCTTGTCAACAAAAGGTTAAAGTTTCTATTTACATAGATCTACGTCTCTATTG
 ATTCCCATGGAAAGAGCTGGGATAGAGAACCCGCCACATGTCTTGCGACCCCTGTTG
 [C, G]
 CTAGGTACATATGATCAAAACCTAGCTAGACAATTGGTTGCTGTGATGAGTGTGAAGT
 TCTCTAAAGATGGCTACTGGCACAGATTCTAAAGGCCCTGTTACACACCTGAGCCT
 TCTCTAGGACCTTCCAGCAGAGGATCCACGGGCTCTGTTGAGAGGTTTC
 CGTTTCTTCCTCCCTATTCTAGGTGATAGAAGGCCCAATGGACCAAAACT
 GCCACAAATACTGAGACGGTATTCTGAGCCTACCATGGACTCGGACTCTACATGCTCT
 23582 TTCTGGCTGACAACCTTAAACAGGTTAGGCACCTGGTAAAAAGAAAAAAA
 ACCAGAGCGAGAACATGGCAAAGATGATTGAAGTTTGTAGGATTTTCTAAATCAG
 CTTTGTCAACAAAAGGTTAAAGTTTCTATTTACATAGATCTACGTCTCTATTG
 ATTCCCATGGAAAGAGCTGGGATAGAGAACCCGCCACATGTCTTGCGACCCCTGTTG
 CCTAGTACATATGATCAAAACCTAGCTAGACAATTGGTTGCTGTGATGAGTGTGAAG
 [T, A]
 TCTCTAAAGATGGCTACTGGCACAGATTCTAAAGGCCCTGTTACACACCTGAGCCT
 TTCTCTAGGACCTTCCAGCAGAGGATCCACGGGCTCTGTTGAGAGGTTTC
 CGTTTCTTCCTCCCTATTCTAGGTGATAGAAGGCCCAATGGACCAAAACT
 GCCACAAATACTGAGACGGTATTCTGAGCCTACCATGGACTCGGACTCTACATGCTCT
 CCTTCTGGCTTCTGGTGTGTTTCTAGGAAACCTCCAGGCCCTGTCCATCT
 24977 TCCATGAGTTATGACAACAAAATGTCCTCAGACATTGCCAACCTTCTGGGGGCAA
 AATCGCCCCCCCACCCAGGGGCACTGGTTAGGTTTCTTCAATTAGATGGTTAATTC
 TGATCATTGATACAGTGGAAAATAGAGGAAATGGTAAAGATTAAAATAAAAATAATT
 TTCTAACCTGTATTAGATAAGTAATTCTTATCAACTCCAGTTAATTGTTATTGTC
 AAATTATAAAATTCACTTGTCTGGCTCACTAACCCATGAGGCAAGTGTGGGGT
 [G, A]
 GCATGAGAGAGAACATCTGTATACAGATGGTAGGAAATCAGGCTGAGAAAAATGTGCC
 TTAAAGACTATGGCTTTGTGAAAATAGAGAATGCAATTCTAAGGCTTGAGAAAAGGAA
 AAAGTAAAGCGGTAATAAAAGCATAACTTAAAAAAATACTTAAATTCACTGTC
 CCCAAATAATTCACTAGTACATATTCTAAAGATGAGAACACAAATACCTCTGAAT
 ACCATGTCCTCCACCCGAGTCTCTCAGGGACCCGCTGTATGTGATTGGTGTCTCA
 25131 TTGTTAAGATTTAAATAAAATAATTCTAACCTGTATTAGATAAGTAATTCTTAT
 CAACTCCAGTTAATTCTTATTGTCAAAATTATAATTCACTGTTCTGCCCTCACTT
 AACCATGCGAGGAAGTCTGTTGGGCTGAGAGAGAACATCTGTATACAGATGGGTA

FIGURE 3W

FIGURE 3X

27423 ATGGTAAGACCTCACTTAAATATCATGGATACATTCTTAGAAAATGCAATACATTAATGT
 ATGTATAGCGGAATCAGTTTCTCATCAATGTTATAACAAAACAGCGTTGAAGGAAG
 TGACTGTAGCTCATTTCAGTTAAAGTCTAGTTCCAAGAACATTATTGACGACAAGGGAG
 GACTTACTGTGAGAATTGAGGAGATATGTTAAACAGACGCTGATTAAACATGTAT
 GTTTCTTATAAATTAACCTTCTCATTTAGTTGGTGGCTAGTAGCAATCAGTAAGT
 [G, A]
 TGTAGAATAATACACTTCTGCTGGCTCATTCCCAAATATCCCCACATATGGATTG
 TGAAAATCCAGCTGACTGTTAACTGATCTGATGTGATAAAGAGCAGGAGTCATT
 CACTAACACAGATAGCACCTGTTCCAATAACTTAGGTTACATTGTGACTCAGGAAT
 AATTACAGGCCACTCTGCTCTAAGTCCATTGTAAGGAAAATACCTTACCCCTGT
 CTTCATCCAGGTATTGAAATGCTTACAAGGGACTAACAGATTCTTAGCAGGGAG
 27735 ACACCTTCTGCTGGCTCATTCCCAAATATCCCCACATATGGATTGAAATTCCA
 GTCTGACTGTTAACTGATCTGATGTGATAAAGAGCAGGAGTCATTCACTAACAC
 AGATAGACCTGTTCCAATAACTTAGGTTACATTGTGACTCAGGAATAAATTACAGGCC
 ACTCTGCTCTAAGTCCATTGTAAGGAAAATACCTTACCCCTGTCTTCACTTCAAG
 GTATTGAAATGCTTACAAGGGACTAACAGATTCTTAGCAGGGGCCAGGGAAAC
 [G, A]
 CATTTTAAATTTTATTTTCAAAAGCAATTAACTACTGCTTGAATCTTCAAAG
 TGAAAGCTGTATAGAGCTTAAATGGATCTCTTACTGCTGAAATTATCTGAA
 GCTGTTAAAGACGATGCCCGTATTATCCAATAGCCATACTGGAAATCAATTAAAAA
 CATTGTAAGGAGCTTTAACATCAATTTTTATTAAATGAGCAACATACATGTG
 GTTTAGAAAACCAATTGTAAGGAGCAGCAGCTTGAATCCCTCCACCTGC
 29875 GTATTAGACTCTCTTAAAGAGATACTGGATTGTTAAAAGGTATGACCTCTCGAT
 TCAGAGCTTAAATCTGAATTCTGTATAGCTTTGCTTGTGTTGCTTCTGCTTCT
 AGAGGATCCCAGGCCACCTCCCTGGGCCCCCTGGAAAGACCTACCCCTCT
 TCTTGGCACAGGATTTTTCACTGGAACTGGATGGAAGAGCTGACTGTGAT
 TTGGCTAGTGTCTCTGGTCCCTGGTCTCAGGTCTGTTCAAGGAATGCTGAG
 [C, G]
 AAACATTGTTAGAAAGTATCTCTGAGGGCAGGCTAGTGCTCACGCTGAAATCTCAG
 CACTTGGGAGGCTAAGCTGGTGGACTCTGGGTTAGGTTAGGAGTCGAACACGCCG
 CAACATGGTAAACCCCTCTACTAAATATACAAAAATCAGCTAGGCTGGGACA
 CGCCTATAACCCAGCCTCGAGGAGCTGGAGGAGAATTGCTTGAACCTGGGAGAC
 CGAGGTGAGTGGCAAGATCACGCCACTGCACTCAGCCTGGTACAGAGCAG
 30356 CGCCTATAACCCAGCCTCGAGGAGCTGGAGGAGAATTGCTTGAACCTGGGAGAC
 GGAGGTGAGTGGCAAGATCACGCCACTGCACTCAGCCTGGTACAGAGCAG
 TCTGCTCaaaaaaaaaaaaaaaaaaaaAGAAATTCTCTGTAACTCAGCTGAGTAA
 GTAAATGTTGCTGGGATTCCATTGAGATCTGGCTTCAACTTTCAAGAACATT
 ATATGAAATTAAATGTTAACATCAAGGCCCTCTACTGCACACTCATCTCTATGT
 [G, T]
 TGCACTGAAAGATGACATATGCAATCAGGAAGGAGGGCTAGACTGAGCTGACATGG
 GGGTAAGTCTGGCTCCATAGAGTAGCTGTGACCTTGAGCAAGGGCTCATCTCT
 TTGACCTCTTAAATTGTTCTGAAAGTGAGCTTAATGATTCTGAGTTAATAGGATTA
 AATGAGATATGTCAAATGCTTGCACAGGCCCTGACATGTTAAATGTTAATAGAT
 TTTATTTTAAATTAATGTTAAATTGAAATCAATAATGCAATAATTCTC
 31344 GTGATCACATGAAATCACTGGTCTCCCTGGGTTTATACCTTGCCCTGTGCTCTATCT
 TAGGCTTCTATGCCATGAAGAGTGTCACTGTAATTCAAAACACAAATGGTTCT
 CTGCTGCTGGGAGGGCTGAAGTGGGACATCTCAGCAGTGAGAAAGAGATCCAA
 GAATCAGGACTGAAAGAGGGCTGAGAAAGTGTGAAAGATGCCCCAGAGACCTTAG
 TTCTGGCATCTAAGGGACCTTGTGCTTAATTTAGTAGCTTCCCTAAGCACAG
 [C, T]
 GCAGAAATTGTTGCTGGTTTATACCAAGACTGTACACAAAGTTATTCTGCAAC
 ATATTGTTTCAAGATTCTTGTATTCTATTAACTAATAGAGGAGGAAACACTG
 CTAGATTGACTCTTAGTTGGATCTAGGGCTGTGCTTCACTGGCTGAGATGCCAG
 GCTGACACTGTATTACCGTGTGCTGGCTCATGAGCTGTCACAGGCCAGATATGG
 GCTCCCTGCCCTCTGGCTCTTGTATTCTGGTATGATGGAACACTGACAGATACATTAG
 32570 GGGCTCTGGTGGCATGTGGCTCACTCACAGGGCAAGGGACATCTCCAGCCTGCAGG
 GATCCTGAGCAGGAGGAGCAGAGCACTGGCTGAGGCCAGGGAGTCCCTGGCTGCTG
 TCCACCCCTACTTTAGGACTCTCTAGCTAGGAGCTGGGCTGAGATCCCTCTAGTCC
 CAAGAGCTAACCGTGTGAAATAACCTTATTAAAGAGCAGATGCTTCTGGAAAT
 TCTGGGATAAAAGAGTTACTTTCTGAGGTTTTTTCTGGCATTAACTT
 [T, G]
 CTGGACTTCTCTCTCTACTACTCTCATAGTTCTGCCCTGGAAA
 CTTTTCTGCACTTCTCTCTACTACTCTCATAGTTCTGCCCTGGAAA

FIGURE 3Y

CAAAATGAAGGATCCTCGGAAGTCTCCACTCATCTGTACCTGGGCATGGTCATCGTCAC
 CATCTCTACATCAGCTGGGTGCTGGGTACCTGCAATTGGAGCTAATATCCAAGG
 CAGCATACCCCTAACCTGCCAACTGCTGTCAGTGGAGGGAGATGGAACCTAGGAG
 CACTGGATTTAAAAAAATAGGGTACAGTGTGGATTCTCCCTTACTTATCTCT
 33220 CTCACTGGCTGCCCTGGACTGATTCTGTTGGGAATTCTAGTAGAGGCTCTGCTGAA
 GCCATTGGTGCTGATCAGCCGATGGGAAGGCATTCTCTGGAACTCTTAAGCTCAGA
 AGGACCGAGTATCTAGTCATTCTAGTGGTAACCTGCCAAATAGACAGGGAGATGGGAGG
 GCAAACGGTACCTGGTACCTGGCTGAGTGGCTCTCCCTGGTAGTAAACGGCTG
 ATATGAGATGGGAGCATCTACTGTGAGCCGGGATTGGGGAGTCCTTGTACCTC
 [T, C]
 CTTGCAATTGGTAATGTATTAGGGAAATAGTGAGGCCATTGAAATGCTCTGAAAG
 GGTGAATGTCCCAGGGCATGTCAGAGCAACCATCTGTTGAAGATGAAATCATCTCAT
 GGTGGAGAGCAGCTGTAGCAGACACTGAGAAGCTTGTGAGTGTCTGGGAGATGAAAT
 GAGCTCTAGTCTAGGGTGTGCTGCTGGGTGCTGTTTATTTGTTGATTGTT
 TTTTATTTATTTGTTTAAAGACAACAGCACTCAGTATTCAGGGCTTCCGTTCAAG
 [T, G]
 CATTGGTGAATGTATTAGGGAAATAGTGAGGCCATTGAAATGCTCTGAAAGGGT
 AATGTCCCAGGGCATGTCAGAGCAACCATCTGTTGAAGATGAAATCATCTCATGGT
 GAGAGCAGCTGTAGCAGACACTGAGAAGCTTGTGAGTGTCTGGGAGATGAAATCAGC
 TTCTAGTCTAGGGTGTGCTGCTGGGTGCTGCTTATTTGTTGATTGTT
 ATTTATTTGTTTAAAGACAACAGCACTCAGTATTCAGGGCTTCCGTTCAAG
 AAATTCCTGAAATGTTCTGCCCTCCAAGAAGGAAGGGCAGGTGGTAGCTGGTAAAC
 33525
 34589 CATGAGGGCTGGTTAAAGGTGGAGCTTGTAGGGACAGAGACCTTCTTTAAATGA
 CCAGGTAGATCTGAATTGATCACAGACTGTTTCTACTCTGTGCACTCAAGGCACT
 GGAGTAATAAAAGGGATATCTGGTGTAGCTGTTGGATGTTGGCTCTGGCTCT
 AGCAGTAGTAGGAAGAGGCCATAGGGTGTGAAAGATGGAATTCTGCTCTGGCTCT
 GGTCTGCACTGTCCTCATCTAATTCTAGGGCACTGACTGGATGGGAGAGATAAAT
 [A, G]
 GGCTTGACATTTAATTGCAATTGTTTATTTGAAGGCATGTACACCTGTATG
 CCCATGGCAAAAGATTGAGATTCAAAAGGTATAGAGACCTTAAGGCTTCCACCCCG
 GCCCTCAACTCTAGTCCCATTACATTTCCTTCAAGGCCATATTCCAG
 TTTCTTTTGTGTTGTTGTTGAGATGTTAGTGTATGATTGTATGTGCTGTTG
 AGTGTGTTGTTTCTCCCTCTTTTCTTAAAGACAATTGTAGCACTCTGTAGGT
 34832 CTCAGTGTCTCATCTAATTCTAGGGCACTGACTGGATGGGACAGATAAAATGG
 CTTGACATTTAATTGCAATTGTTTATTTGAAGGCATGTACACCTGTATGCC
 CATCACCAAGATTGAGATTCAAAAGGTATAGAGACCTTAAGGCTTCCACCCCGCG
 CCTTCAACTCTAGTCCCATTACATTTCCTTCAAGGCCATATTCCAGTT
 TGTTGTTGTTGTTGAGATGTTAGTGTATGATTGTATGTGCTGTTG
 [G, T]
 GTGTGTTTCTCTCTTTTCTTTAAAGACAATTGTAGCACTCTGTAGGTACT
 GTATTGCTTCTGCTTTTCACTTAAAGGTATAGAGCTGCCCCATGATAGTG
 ATATGCTATATCATGTGATAGGTATATCATGGGATAGTTCTATCACACCATCA
 CACCTAGATCTGCTCATCTTGTAAAGCTATACGGGGCACACGTTACCTA
 TCGAGTCCCAGTGGTAACATTAAATTGTTCTAGTCTTCTTAAATAATGCTG
 35188 GTAGCTGTTGCTCATGCTTTTCACTAAAAAAAGTATATAAAACTGTCCCCCATGA
 TAGTGTGATGTGATATCATGTGATAGGTATATCATGGGATAGTTCTATCACAC
 CATCACCACTAGATTCTGCTCATCTTGTAAAGGTATACGGGGCACACGATT
 ACCTATCGAGTCCCAGTGGTAACATTAAATTGTTCTAGTCTTCTTAAATAA
 TGCTGAGTGTGAGATATTGAAATATAAGCTTGTGATGTGTTGAGGATATGTGAG
 [A, G]
 TAAATTCTAGACATGAAATTGCTGGTCCGAAGGACATGGGGTTGTATCTTGATAA
 GTGTCACAAATGCCAATGGGACCATTTGCACTCTGTGATGATGTTAAGTGTG
 AGCAGGGTGGAAATGCTCTGTCTGCTGGCAGGGTGTACCTGAGTCACTGCTG
 TACTCCATGGGATCTTTCACCTACGCACTCCAGTCTACGTCGGCTGAGATCATC
 ATCCCCCTCTTGTGTCGGAGGCCCCGAGCACTGTGAGTTAGTGGTGGACCTGTTG
 35614 GCTTGGAAATGCTCTGTGTTGGCAGGGTGTACCTGAGTCACTGCTGACTC
 CATGGGATCTTTCACCTACGCACTCCAGTCTACGTCGGCTGAGATCATCATCC
 CTCTTGTGTCGGAGCAGGCCAGCACTGTGAGTTAGTGGTGGACCTGTTG
 GCAGC

FIGURE 3Z

	AGTGTCTGGCTGCTGACATGTGAGTAGAAGATGATAATTGCCCTGCTTGTCCCCCTAAAGGGCACCCAGTCGAGGCTTCACTGAGAAAAGACAATGTGTGTGTAGTGAAAGCTGG [G, C]
	TATGTTGTGACAGAGAACCTGGCCCATGGCTCACTTCAGAGTTGAGGCACCTCCAGA TGGGAAAGTGAATTAAATTACATATGTAAGGAAACATGGGAATGAGGGACAGTGGTT ATGTATAGATAGGGTATGAAGTGTGGAGGTTGTTATCCTCAGATAAGGACATGG ATTACTATCCCATATAAATAGGTAAGGCTGAAAGGCCATTAAACCATATCTGAAT GAGTATAAGTACTCTGTGAAAGGGTACTTATTGCTTTCTAAATAGTTTCCAC
37852	TTTAAACAGCAGCTCTTATTACTATTCGGTGTCTTCTATCTTTCCCCAACCTT TCCCTCTCTTCAACCTCCAAGGAAACAGGGAATTCTAGTGTAGTTCTTTTT TTCTCTCTTGGAAATTCAAACCTTCAACCTCTCCCCTATCTTCAAAAGTACTATGG CTGATACGGATTGTGTGTTAATTCACAGTTGGAGAAGAGGGGGAGGAAACAA AGTATTCATAGGATAGTGTCTTATTTGTATGATTCATCGGAGCTATCTACTTCC [C, A] GCCCATATTGGAAATGGGACTTAGCAGGTACCTTATGTCCAGACCTTGTGTGGAA GAGGCTGGCCCCACCTGTGGAGTGTGGAGTGTAGGATCACGGTTTTTATGTTTCTT GGAGCAATAACCCATCCATCTTCACTGTTAGTCTACATGTTCTGTGTCTTGGCATG TGAACATTCTTACTCTGGTCTGATAAAGTTTCAAGAACCTATTCTGAAGATATAAT TACCTAAATCGCATCATCCAAGAACCTGTTCAACTGGAATGAGCTGCAAACAT
38643	GTCTCACTGTAAGATAGGAAGGGTGTCTGACCTCTAAGGTTTCTCAACTCCAAAAT TCTGTGATTCTGTATAGGTGTCTTGGCTGATTAAAGTTCTACAAACATTACTTAA AAAAAAAGAAGTCATGTAACATTTGGAAATAAAGAAGAAATTCACTGATTCCAC CAATTAAACAAAGTAATTTTTTGCTATTGTATCTCTGTGTCTTAACCTCATGGGTG CTTGTAAAATAGTTGCAATTGTAAGTTACACATAATTGGTCTTCACATTATTTA [G, A] TTTATATACAAAATATTCAATCTTCACTAATATTGCTGACCTCGTGTATTCCAC TGTATTGGTGGATCATATAACTAAGGTCTCTTCACTGTTGACATGGTGTGTTTC CTTGTGTTCTGATTTTTAAATTATACCCCAACTAAGTCAACATTGTATACTGTCCA AGACTGTGAATTAAAGGCAATTATAGACATTTAAAGTAAACATGGTGAACACC CGTCTCTACTAAAATACAAAACAAAATTAGCTGGTGTGGCAGGTGCTGTAGTC
39198	ATACAAAAAAACAAAATTAGCCTGGTGTGGCAGGTGCTGTAGTCCCAGCTATTGGGA GGCTGAGGAGGGAAATGGCATAAACCCAGGAGGAGCTGGCAGAGCTGGCAGGAAATGCG GCCACTGCAAGCCTGAGTGCACAGGGCAGACTCCATCTCAAACCAATAAAATAA AAATAAAATAAAATAAAAGTAACCTGGTAAGTTTAAACAGTTGATCATATAAA ATAGCAGCAAGAGTCCCAAGCACAGGAGGCTAAATGGCAGGCTGGTCAAGTGG [G, T] TTTGTCTTTCAGTGTCTTGTGTTGATATAAGTCTGGTCTTGTGACTCTTGTGATGCTGGTT CAAACCCAGGCTTCAAGAACCTGGTCTCTTGTGAACTGACTGTTGGCTTATGTTG CTCAGGAGTTAAAGCTCATTTTGTGTTGACTCTGACTCGAAGGGAAAGTGTGTT TAATACTGGAGCCCTTGTGACTATCATGTGTTGAGCTGGTGTGAGAAGTGTATAACTG CCCTTTGTACAGGCCACAGCTGAGCTGGTGTGAGAAGTGTATAACTGCTTGTATA
39550	ATGCTGGTCAAAACCAAGGCTTCAAGATCCAGTCTTCTGTGAAACATGACTGTTGG CTTATGTTGCTTCAGCAGTAAAGCTCATATTCTTGTGCTCTTGTGACTCGAAGGGAA GATTTTTGTAATACTGTTGAGCCCTTGTGACTATCATGTGTTGAGCTGGTGTG CTCTGTCCCCCTTTGTACAGGCCACAGCTGGCTGCTGTGAGAAGTGTATAACTG TTTGTATACAAATGCTTCTTTGTCTGGCTGGGCTTGTGTTGTGTGGGGGGGG [T, G] GATTAGGGAGAGTAGGGAGAGGGCTGTTCTGGCTGGCTGTTCTGAGATATCTACCT TGTGAGTGTCTTCATAGGCACTTAACACAGAAAGACATTAGTGCAGAAGGGG TTTATTTGGCCACCATGTGCTGATAGTGTGCTGTTCTGGAGTTGTAAGTAAAGCT TTCCATGGTGGCAAAACAGATACCGCTGTGTTGAGCTGGGCTGGTGTGAGTGT TGGTTGGACATCTTCTCTTCTCCACATTGTGTTAGTGGAGGCTGCTCTTGTG
42281	GCACAGCTCCAGGTTAAAGTGTGAGGAGGGCATGAATCCATTCTTCCCCGGTGTGTT AGTCATTTGGCTTATAAAAGGAAACACTGAGACTGGTAATTATAAAAGAAAAGGG TTTATTTGGCTCATGGCTGAGGCTGATACAGGAAGTGTGTGAGCTGGCAGCTGTCTT GGTAGGGCCCTCAGGAAGCTTCAATCTGGCAAGAAGGGGGAGGAGCTTATA TGGCAAGACAGGGAGCAAGGAGAAGGGAGGTTACAGGCTCTTTAAACACAGCTCTC [A, G] GGGAGGGCCCCAAAGTCTGAGGGATTGGCCCCACGACTCAAACACTTCCCACAG GCCCCACCTGACATTGGGATCACATTCAACATGAAATTGGAGGGATCCTAACCA TATTACTGGTAAAGTCTTGTGTTCAACATGCTCTCATCTTACTGAGGGAGTGT TCTTTGTTGTTGTTGCTCTTCAAAATCAACTTGTAGACATTCTGGAGTTAAAGTGT TCTTAAAGTCTGCTCTTCAAAATGCAATCTGGCAAGAAGGGGGAGGAGCTTATA

FIGURE 3AA

42321 CATTCTTCCCTGGTGTAGTCATTGCGTTATAAAGAACCTGAGACTGGG
TAATTTATAAAAGAAAAGAGGTTTATTTGGCTCATGGCTGAGGCTGACAGGAAGTG
TGATGCCAGCTGCTTCTGGTGAAGGCCTCAGGAAGCTTAAATCATGGCAGAACGCA
AAGGGGAGCAGGTTTATGGCAAGACAGGGCAGGAAGGAAGGGAGTACAGGCTC
TTTAAACAAACAGCTCTCAGGGAGGCCAAGTCATTGAGGGATTTGCCAAC
[G, A]
ACTCAAACACTCCCCACAGGCCAACCTGACATGGGATCACATTCAACATGAAA
TTGGAGGGATCCAACCATATTACCTGGTAAGTCTTCCACATGCTCTCATCT
TACTGCAGGGAGTGTCTTCTTTGGTTTATGGCTCTCAAACATCAACTTTA
GACATTTCAGTTAAAGTGTCTTAAACATCTGGCTCTCAAATGCAATCCAATCTTCA
GCTGCTAGCAGGAAAGAACAGTCATGATGAGCATGGCTGCCCTGGACTGAGATGTT
42563 TTAACAAACAGCTCTCAGGGAGGCCAACGTCATTCAATGAGGGATTTGCCAACGA
CTCAAACACTCCCCACAGGCCAACCTGACATGGGATCACATTCAACATGAAAT
TTGGAGGGATCCAACCATATTACCTGGTAAGTCTTCCACATGCTCTCATCTT
ACTGCAGGGAGTGTCTTCTTTGGTTTATGGCTCTCAAACATCAACTTTAG
ACATTCAGTTAAAGTGTCTTAAACATCTGGCTCTCAAATGCAATCCAATCTTCA
[G, C]
TGCTCAGGAAAGAACAGTCATGAGCTGAGACATTGGCTGCCCTGGACTGAGATGTTCT
GGCAGTCTACCAAGTGTGGCTCTTCAAGTGCATTGACTGCATTTCGCTTACAG
AATGAACCTAGAACGAAACCTCTCATATAAAATGAAACCTCTCGTAGGAATCAATGAGG
TAGTAGAGTCAGCTGGATGTCTGATCAAGGCTGGAGCATCCAGCTGAGGCCAGCAG
TAGGAAAGACAATCTGCAAACTATTTGATTGCTAAGGTTAGTAACAGGAAG
42675 CATGAAATTGGAGGGATCCAACCATATTACCTGGTAAGTCTTGTCTTCAACATGCT
CTCATCTTACTGCAGGGAGTGTCTTCTTTGGTTTATGCTCTCAAACAT
AACTTACAGCTTCAGTTAAAGTGTCTTCAAACATCTGGCTCTCAAATGCAATCCA
TCCCTCAGCTGCTCAGGAAAGAACAGTCATGAGCTGAGACATTGGCTGCCCTGGACTG
AGATGTTCTGGCAGTCTCAGGTCAGTGTGGCTCTTCAAGTGCATTGACTGCATTTC
[G, A]
CTTTACAGAATGAACCTAGAACAAACCTCTCATATAAAATGAAACCTCTGAGGAAT
CAATGAGGTAGTAGATAAGCTGGATGTCTGATCAAGGCTGGAGCATCCAGCTGAG
CCCAGCAGTAGGAAAGACAATCTGCAACACTATTGATTGCTAAACAGGTTAGTAACCTA
ACAGGAAGTCATGACTGAGCTGAGGATGACTTTCTGGCCAAAAAGATGAGTACTAAT
GATGATAACATTAACAGGTAAGACATCCTACTGTACACAGGCCCTTGTGAGGACCT
42908 TGGAAGTGGAGATTTCTGGCAGTCTCAGGTGTGGCTCTTCAAGTGCATTGACTG
CATTTGCCCTTACAGAATGAACCTAGAACAAACCTCTCATATAAAATGAAACCTCTC
GTAAGAATCAATGAGGTAGTAGATAAGCTGTGGATGTCTGATCAAGGCTGGAGCATCC
AGCTGTAGCCCGAGCAGTAGGAAAGACAATCTGCAACACTATTGATTGCTAAACAGGTT
AGTAACAAACAGGAAGTCATGCACTGTAGCAGGATGACTTTCTGGCCAAAAAGATG
[G, A]
TAACTATGATGATAACATTAACAGGTAAGACATCCTACTGTACACAGGCCCTTGTGA
GGCACCTGCTACAGGAAACCTTACGGCATCATGACATCTTATGATTCAAGGAGCAGTTAATA
TCCCCATTTGCCAAACGAAACCTGGGAATAGAAAGTACCATACCTTCCCAATGTC
ACTCAGGAACTTAGCAGCAGGCCAGGATCTGAACACAAGAACCTAGTCCAGAGGCCAC
AGGGCTCAATAAACCTGTAACACTGGCTTCTGCCACCTGGTGGAAAGATCGGTGAGA
43358 AATAGAAAGGTACCATACCTTCCCAATGTCACTCAGCTAATTAGCAGCAGGCCAGGAT
CTGAACACAAGAACCTAGTCCAGGCCACAGGCCCTAATAACACCTGAAACACTGGC
CTTGGCCACCTGGTGAAGAGTCGGTAGAGTGGAGCTGGGTCACTGGGCACTAGG
ATGGGTGATTCTGGTGAAGCCTCTCTGCTCATAGCAGTGTGGCAGTGTGACAATG
GCTGTTATGGCACCGAACGGCGTGGCACCTCTGGCAGTCACCATTTGGTCTTGTCA
[-, G]
TTCCCTTCTGGCTACCCGGCTGAGTTTCAGATGTGAGAGCAGTGGGTGCTG
TCACAGAGATACGGCTGCTGTGGGGCTTCGCCAGGGTCACTGGCAGATAGAACCTG
TTTTTTCACCTGTATCAAATGCTCTGTAAGTGGTTTATCACGGTGTCTTCCAG
AAGGGGGGTTTCTTCTGTTGGTCACTGGTCAAGGCTGGAGATGTTGTGTTGG
AGGCTCCCTGAGTGTAAAGAAAATGAGCAGCTGCTCAGGAACGTCACCTCCCTTCTC
43371 CATACTTCCCCAATGTCACTCAGCTAATTAGCAGCAGGCCAGGATCTGAACACAAGAA
CTAGTCCAGGCCACAGGCCCTAATAACACCTGAAACACTGGCTTGGGCCACCTG
GTGAAAGATCGGTGAAGATGGGAAGCCTGGGGTCACTGGGCACTAGGATGGGTGATTG
GTGAAGGCCCTCTCTGGCTTACAGCAGTCAGTGTGGCAGTCAGTGGTGAACATGGCTGG
GGAGGCCATGGCACCTCTGGCAGTCACCATGGTCTTGTCACTGGCTTCTC
[G, C]
GCTCACCCGGCTGAGTTCAAGATGTGAGAGCAGTGGGTGCTGTACAGAGATACG

FIGURE 3BB

Docket No.: CL001062CON
Serial No.: TO BE ASSIGNED
Inventors: WEI, Ming-Hui et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

GTCGTCGTGCGGGCTTCGCCAGGGTCAAGCTGCAGATAGAACTGCTTTTTCACCTG
TATCAAAATGCTGTGAAATGCGGTTTACAGGTGCTTCCAGAAGGCGGGTTTC
TTTCTATTGGTTCTTGTCAGTCAGGTAGAGATGTTGTGTTGAGGCTCCCTGAGT
GGTAAGAAAATGAGCAGCTGCTCAGGAACGTCACCTCTTCTCTCCCTACCCCTCCC

44796 GGCATCGCTACCTGTACCTATTTACACCCAGAACCTTCAGCTCCCCCATCATGCCT
CCTCCCTCTACCTGCCTCCCTCTGCTGGTGACCTCGCCAACCTCTTACTGCAC
AGTTCACTTATTAAACAATTTCTGCCCCACCTCATGTTTACCCCTTACTGGC
CAGGCATAGATTAACTGGGAACGCCCTCTTATAAAAGCTGGCTCTTCTCAT
CTCTCCCAAATGTTGATACTCAGTATTCTCTTATTCAGTCTCAGGGGTGGCT
[G,A]
ACCTACCTGGTCAATTGAAACAGGCCCCAACAGTGGAGTTTTAATCTGGACTCTCTGGC
TTGCTGTGACCCCTAAAGGAATGCTCTTCCCTGGTATTCCTTAGTGTGGTCAAGT
ACTGTTCTTAGTGTCTTAAACATCGAAGTGTGCTTAAACTGAAATA
TTTATCTTTTATTAAATCAGATTTGTTTAACTGCTTAAACTGTTAGATCTGGGTATTA
CGAACATCTCTCTCAGTAAACTTGAACACTTCTCTGCTGAAAGAAGCTCGCT
[A,G]

45820 GGGAAAAGGGCAGAACCACTGCCCCGGCCACACTGCCTCTGTCGGCTGGACTTTGAAAG
GAACCCACTGAACACTAATTATGAGCCCTGCTTCCCTGGTATTCCTTAGTGTGGTCAAGT
ACAAACAGCCTTGAGGTTGGCCCTCTCAAGGTCAAGCTCAGATTTGGGAGCAAACCTC
AGAGAAAGGAGAGGAGAACATTCAGCTGTGGCTGCCTCTCTTCTCTGGT
TGCAGAATTTCAAGGCAATTGATGAATTCCCTCTTAGCTGTGTTAGCTGAC
[A,G]
TGTGTGTGACGTGCGTGTGTGTGTTCTGTGTAAGTAACAGACAGAACACTCCTTT
CTCTTCTGTCCCGTACCAAGGCTCTGCTTCACTGCAGATAACAGTTCACTCTGAAAGCTG
GTTGAAGGAGAGCAGAAAAATGATCAGGGTTTGTCTCTGTGTTTGCCAAAGCTCA
TAAGGGCTGTGACCCACCCATATGCCCAAGTTTCTGCTCTCTGTTCAAAGCCA
GGAGAGCTGACTCCAGGTGAAGGGATGGAAAAGTGGACTCTCATTTGACTGCCA

FIGURE 3CC